

SEQUENCE LISTING

<110> Ballinger, Dennis
 Loeb, Debra
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 Qian, Xiahong
 Wang, Dunrui

<120> MATERIALS AND METHODS RELATING TO LIPID METABOLISM

<130> 28110/35915A

<150> US 60/197,137

<151> 2000-04-14

<150> US 09/714,936

<151> 2000-11-17

<150> US 09/667,298

<151> 2000-09-22

<150> US 09/631,451

<151> 2000-08-03

<150> US 09/598,042

<151> 2000-06-20

<160> 45

<170> PatentIn version 3.0

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Asp	Lys	Gly	Arg 40	Val	Glu	Gln	Ile	His 45	Gln	Gln	Lys	Met 50	Ala	Arg	Glu	
ccc	gcg	acc	ctg	aaa	gac	agc	ctt	gag	caa	gac	ctc	aac	aat	atg	aac	249
Pro	Ala	Thr 55	Leu	Lys	Asp	Ser	Leu 60	Glu	Gln	Asp	Leu	Asn 65	Asn	Met	Asn	
aag	ttc	ctg	gaa	aag	ctg	agg	cct	ctg	agt	ggg	agc	gag	gct	cct	cgg	
Lys	Phe 70	Leu	Glu	Lys	Leu	Arg 75	Pro	Leu	Ser	Gly	Ser 80	Glu	Ala	Pro	Arg	
ctc	cca	cag	gac	ccg	gtg	ggc	atg	cgg	cgg	cag	ctg	cag	gag	gag	ttg	345
Leu 85	Pro	Gln	Asp	Pro	Val 90	Gly	Met	Arg	Arg	Gln 95	Leu	Gln	Glu	Glu	Leu 100	
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Glu	Glu	Val	Lys 105	Ala	Arg	Leu	Gln	Pro	Tyr 110	Met	Ala	Glu	Ala	His 115	Glu	
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Leu	Val	Gly 120	Trp	Asn	Leu	Glu	Gly	Leu 125	Arg	Gln	Gln	Leu	Lys 130	Pro	Tyr	
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Thr	Met	Asp 135	Leu	Met	Glu	Gln	Val 140	Ala	Leu	Arg	Val	Gln 145	Glu	Leu	Gln	
gag	cag	ttg	cgc	gtg	gtg	ggg	gaa	gac	acc	aag	gcc	cag	ttg	ctg	ggg	537
Glu	Gln 150	Leu	Arg	Val	Val	Gly 155	Glu	Asp	Thr	Lys	Ala 160	Gln	Leu	Leu	Gly	
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Gly 165	Val	Asp	Glu	Ala 170	Trp	Ala	Leu	Leu	Gln	Gly 175	Leu	Gln	Ser	Arg	Val 180	
gtg	cac	cac	acc	ggc	cgc	ttc	aaa	gag	ctc	ttc	cac	cca	tac	gcc	gag	633
Val	His	His	Thr 185	Gly	Arg	Phe	Lys	Glu	Leu 190	Phe	His	Pro	Tyr	Ala 195	Glu	
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Val	Ala	Pro 215	His	Ala	Pro	Ala	Ser 220	Pro	Ala	Arg	Leu	Ser 225	Arg	Cys	Val	
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cgc	atc	cag	cag	aac	ctg	gac	cag	ctg	cgc	gaa	gag	ctc	agc	aga	gcc	825
Arg 245	Ile	Gln	Gln	Asn	Leu 250	Asp	Gln	Leu	Arg	Glu 255	Glu	Leu	Ser	Arg	Ala 260	
ttt	gca	ggc	act	ggg	act	gag	gaa	ggg	gcc	ggc	ccg	gac	ccc	cag	atg	
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tac ctg cag ata gct gcc ttc act cgc gcc atc gac cag gag act gag 969
Tyr Leu Gln Ile Ala Ala Phe Thr Arg Ala Ile Asp Gln Glu Thr Glu
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gag gtc cag cag cag ctg gcg cca cct cca cca ggc cac agt gcc ttc 1017
Glu Val Gln Gln Gln Leu Ala Pro Pro Pro Pro Gly His Ser Ala Phe
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gcc cca gag ttt caa caa aca gac agt ggc aag gtt ctg agc aag ctg 1065
Ala Pro Glu Phe Gln Gln Thr Asp Ser Gly Lys Val Leu Ser Lys Leu
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cag gcc cgt ctg gat gac ctg tgg gaa gac atc act cac agc ctt cat 1113
Gln Ala Arg Leu Asp Asp Leu Trp Glu Asp Ile Thr His Ser Leu His
      345      350      355

gac cag ggc cac agc cat ctg ggg gac ccc tgaggatcta cctgcccagg 1163
Asp Gln Gly His Ser His Leu Gly Asp Pro
      360      365

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Gln Thr Ser Gly Asp Lys Gly Arg Val Glu Gln Ile His Gln Gln Lys
35 40 45

Met Ala Arg Glu Pro Ala Thr Leu Lys Asp Ser Leu Glu Gln Asp Leu
50 55 60

Asn Asn Met Asn Lys Phe Leu Glu Lys Leu Arg Pro Leu Ser Gly Ser
65 70 75 80

Glu Ala Pro Arg Leu Pro Gln Asp Pro Val Gly Met Arg Arg Gln Leu
85 90 95

Gln Glu Glu Leu Glu Glu Val Lys Ala Arg Leu Gln Pro Tyr Met Ala
100 105 110

Glu Ala His Glu Leu Val Gly Trp Asn Leu Glu Gly Leu Arg Gln Gln
115 120 125

Leu Lys Pro Tyr Thr Met Asp Leu Met Glu Gln Val Ala Leu Arg Val
130 135 140

Gln Glu Leu Gln Glu Gln Leu Arg Val Val Gly Glu Asp Thr Lys Ala
145 150 155 160

Gln Leu Leu Gly Gly Val Asp Glu Ala Trp Ala Leu Leu Gln Gly Leu
165 170 175

Gln Ser Arg Val Val His His Thr Gly Arg Phe Lys Glu Leu Phe His
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Pro Tyr Ala Glu Ser Leu Val Ser Gly Ile Gly Arg His Val Gln Glu
195 200 205

Leu His Arg Ser Val Ala Pro His Ala Pro Ala Ser Pro Ala Arg Leu
210 215 220

Ser Arg Cys Val Gln Val Leu Ser Arg Lys Leu Thr Leu Lys Ala Lys
225 230 235 240

Ala Leu His Ala Arg Ile Gln Gln Asn Leu Asp Gln Leu Arg Glu Glu
245 250 255

Leu Ser Arg Ala Phe Ala Gly Thr Gly Thr Glu Glu Gly Ala Gly Pro
260 265 270

Asp Pro Gln Met Leu Ser Glu Glu Val Arg Gln Arg Leu Gln Ala Phe
275 280 285

Arg Gln Asp Thr Tyr Leu Gln Ile Ala Ala Phe Thr Arg Ala Ile Asp
290 295 300

Gln Glu Thr Glu Glu Val Gln Gln Gln Leu Ala Pro Pro Pro Pro Gly
305 310 315 320

His Ser Ala Phe Ala Pro Glu Phe Gln Gln Thr Asp Ser Gly Lys Val
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atg gga tcc tgg gtg cag ctc atc aca agc gtc ggg gtg cag caa aac 228
Met Gly Ser Trp Val Gln Leu Ile Thr Ser Val Gly Val Gln Gln Asn
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cat cca ggc tgg aca gtg gct gga cag ttc caa gaa aag aaa cgc ttc 276
His Pro Gly Trp Thr Val Ala Gly Gln Phe Gln Glu Lys Lys Arg Phe
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act gaa gaa gtc att gaa tac ttc cag aag aaa gtt agc cca gtg cat 324
Thr Glu Glu Val Ile Glu Tyr Phe Gln Lys Lys Val Ser Pro Val His
35 40 45

ctg aaa atc ctg ctg act agc gat gaa gcc tgg aag aga ttc gtg cgt 372
Leu Lys Ile Leu Leu Thr Ser Asp Glu Ala Trp Lys Arg Phe Val Arg
50 55 60

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Val Ala Glu Leu Pro Arg Glu Glu Ala Asp Ala Leu Tyr Glu Ala Leu
65 70 75 80

aag aat ctt aca cca tat gtg gct att gag gac aaa gac atg cag caa 468
Lys Asn Leu Thr Pro Tyr Val Ala Ile Glu Asp Lys Asp Met Gln Gln

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	85	90	95	
aaa gaa cag cag ttt agg gag tgg ttt ttg aaa gag ttt cct caa atc				516
Lys Glu Gln Gln Phe Arg Glu Trp Phe Leu Lys Glu Phe Pro Gln Ile	100	105	110	
aga tgg aag att cag gag tcc ata gaa agg ctt cgt gtc att gca aat				564
Arg Trp Lys Ile Gln Glu Ser Ile Glu Arg Leu Arg Val Ile Ala Asn	115	120	125	
gag att gaa aag gtc cac aga ggc tgc gtc atc gcc aat gtg gtg tct				612
Glu Ile Glu Lys Val His Arg Gly Cys Val Ile Ala Asn Val Val Ser	130	135	140	
ggc tcc act ggc atc ctg tct gtc att ggc gtt atg ttg gca cca ttt				660
Gly Ser Thr Gly Ile Leu Ser Val Ile Gly Val Met Leu Ala Pro Phe	145	150	155	160
aca gca ggg ctg agc ctg agc att act gca gct ggg gta ggg ctg gga				708
Thr Ala Gly Leu Ser Leu Ser Ile Thr Ala Ala Gly Val Gly Leu Gly	165	170	175	
ata gca tct gcc acg gct ggg atc gcc tcc agc atc gtg gag aac aca				756
Ile Ala Ser Ala Thr Ala Gly Ile Ala Ser Ser Ile Val Glu Asn Thr	180	185	190	
tac aca agg tca gca gaa ctc aca gcc agc agg ctg act gca acc agc				804
Tyr Thr Arg Ser Ala Glu Leu Thr Ala Ser Arg Leu Thr Ala Thr Ser	195	200	205	
act gac caa ttg gag gca tta agg gac att ctg cat gac atc aca ccc				852
Thr Asp Gln Leu Glu Ala Leu Arg Asp Ile Leu His Asp Ile Thr Pro	210	215	220	
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Asn Val Leu Ser Phe Ala Leu Asp Phe Asp Glu Ala Thr Lys Met Ile	225	230	235	240
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Ala Asn Asp Val His Thr Leu Arg Arg Ser Lys Ala Thr Val Gly Arg	245	250	255	
cct ttg att gct tgg cga tat gta cct ata aat gtt gtt gag aca ctg				996
Pro Leu Ile Ala Trp Arg Tyr Val Pro Ile Asn Val Val Glu Thr Leu	260	265	270	
aga aca cgt ggg gcc ccc acc cgg ata gtg aga aaa gta gcc cgg aac				1044
Arg Thr Arg Gly Ala Pro Thr Arg Ile Val Arg Lys Val Ala Arg Asn	275	280	285	
ctg ggc aag gcc act tca ggt gtc ctt gtt gtg ctg gat gta gtc aac				1092
Leu Gly Lys Ala Thr Ser Gly Val Leu Val Val Leu Asp Val Val Asn	290	295	300	
ctt gtg caa gac tca ctg gac ttg cac aag ggg gca aaa tcc gag tct				1140
Leu Val Gln Asp Ser Leu Asp Leu His Lys Gly Ala Lys Ser Glu Ser	305	310	315	320
gct gag tcgctgaggc agtgggctca ggagctggag gagaatctca atgagctcac				1196
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 aaaaaaaaaa 1931

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Thr Gly Lys Met Pro Ile Leu Ser Tyr Trp Pro Tyr Gly Cys His Cys
 35 40 45

Gly Leu Gly Gly Arg Gly Gln Pro Lys Asp Ala Thr Asp Trp Cys Cys
 50 55 60

Gln Thr His Asp Cys Cys Tyr Asp His Leu Lys Thr Gln Gly Cys Gly
 65 70 75 80

Ile Tyr Lys Asp Tyr Tyr Arg Tyr Asn Phe Ser Gln Gly Asn Ile His
 85 90 95

Cys Ser Asp Lys Gly Ser Trp Cys Glu Gln Gln Leu Cys Ala Cys Asp
 100 105 110

Lys Glu Val Ala Phe Cys Leu Lys Arg Asn Leu Asp Thr Tyr Gln Lys
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Cys
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gctgggtggaa cagtgggtg atg gcg tcc ctg ctg caa gac cag ctg acc act	172
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Asp Gln Asp Leu Leu Leu Met Gln Glu Gly Met Pro Met Arg Lys Val	
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Arg Ser Lys Ser Trp Lys Lys Leu Arg Tyr Phe Arg Leu Gln Asn Asp	
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Gly Met Thr Val Trp His Ala Arg Gln Ala Arg Gly Ser Ala Lys Pro	
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Ser Phe Ser Ile Ser Asp Val Glu Thr Ile Arg Asn Gly His Asp Ser	
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Glu Leu Leu Arg Ser Leu Ala Glu Glu Leu Pro Leu Glu Gln Gly Phe	
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Thr Ile Val Phe His Gly Arg Arg Ser Asn Leu Asp Leu Met Ala Asn	
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Ser Val Glu Glu Ala Gln Ile Trp Met Arg Gly Leu Gln Leu Leu Val	
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510 515 520

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Val Gln His Asn Thr Arg Gln Leu Ser Arg Val Tyr Pro Ser Gly Leu
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<213> Homo sapiens

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Met Ala Ser Leu Leu Gln Asp Gln Leu Thr Thr Asp Gln Asp Leu Leu
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Leu Met Gln Glu Gly Met Pro Met Arg Lys Val Arg Ser Lys Ser Trp
20 25 30

Lys Lys Leu Arg Tyr Phe Arg Leu Gln Asn Asp Gly Met Thr Val Trp
35 40 45

His Ala Arg Gln Ala Arg Gly Ser Ala Lys Pro Ser Phe Ser Ile Ser
50 55 60

Asp Val Glu Thr Ile Arg Asn Gly His Asp Ser Glu Leu Leu Arg Ser
65 70 75 80

Leu Ala Glu Glu Leu Pro Leu Glu Gln Gly Phe Thr Ile Val Phe His
85 90 95

Gly Arg Arg Ser Asn Leu Asp Leu Met Ala Asn Ser Val Glu Glu Ala
100 105 110

Gln Ile Trp Met Arg Gly Leu Gln Leu Leu Val Asp Leu Val Thr Ser
115 120 125

Met Asp His Gln Glu Arg Leu Asp Gln Trp Leu Ser Asp Trp Phe Gln
130 135 140

Arg Gly Asp Lys Asn Gln Asp Gly Lys Met Ser Phe Gln Glu Val Gln
145 150 155 160

Arg Leu Leu His Leu Met Asn Val Glu Met Asp Gln Glu Tyr Ala Phe
165 170 175

Ser Leu Phe Gln Ala Ala Asp Thr Ser Gln Ser Gly Thr Leu Glu Gly
180 185 190

Glu Glu Phe Val Gln Phe Tyr Lys Ala Leu Thr Lys Arg Ala Glu Val
195 200 205

Gln Glu Leu Phe Glu Ser Phe Ser Ala Asp Gly Gln Lys Leu Thr Leu
210 215 220

Leu Glu Phe Leu Asp Phe Leu Gln Glu Glu Gln Lys Glu Arg Asp Cys
225 230 235 240

Thr Ser Glu Leu Ala Leu Glu Leu Ile Asp Arg Tyr Glu Pro Ser Asp
245 250 255

Ser Gly Lys Leu Arg His Val Pro Ser Met Asp Gly Phe Leu Ser Tyr
260 265 270

Leu Cys Ser Lys Asp Gly Asp Ile Phe Asn Pro Ala Cys Leu Pro Ile
275 280 285

Tyr Gln Asp Met Thr Gln Pro Leu Asn His Tyr Phe Ile Cys Ser Ser
290 295 300

His Asn Thr Tyr Leu Val Gly Asp Gln Leu Cys Gly Gln Ser Ser Val
305 310 315 320

Glu Gly Tyr Ile Arg Ala Leu Lys Arg Gly Cys Arg Cys Val Glu Val
325 330 335

Asp Val Trp Asp Gly Pro Ser Gly Glu Pro Val Val Tyr His Gly His
340 345 350

Thr Leu Thr Ser Arg Ile Leu Phe Lys Asp Val Val Ala Thr Val Ala
355 360 365

Gln Tyr Ala Phe Gln Thr Ser Asp Tyr Pro Val Ile Leu Ser Leu Glu
370 375 380

130 140 150 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380

Thr His Cys Ser Trp Glu Gln Gln Gln Thr Met Ala Arg His Leu Thr
385 390 395 400

Glu Ile Leu Gly Glu Gln Leu Leu Ser Thr Thr Leu Asp Gly Val Leu
405 410 415

Pro Thr Gln Leu Pro Ser Pro Glu Glu Leu Arg Arg Lys Ile Leu Val
420 425 430

Lys Gly Lys Lys Leu Thr Leu Glu Glu Asp Leu Glu Tyr Glu Glu Glu
435 440 445

Glu Ala Glu Pro Glu Leu Glu Glu Ser Glu Leu Ala Leu Glu Ser Gln
450 455 460

Phe Glu Thr Glu Pro Glu Pro Gln Glu Gln Asn Leu Gln Asn Lys Asp
465 470 475 480

Lys Lys Lys Lys Ser Lys Pro Ile Leu Cys Pro Ala Leu Ser Ser Leu
485 490 495

Val Ile Tyr Leu Lys Ser Val Ser Phe Arg Ser Phe Thr His Ser Lys
500 505 510

Glu His Tyr His Phe Tyr Glu Ile Ser Ser Phe Ser Glu Thr Lys Ala
515 520 525

Lys Arg Leu Ile Lys Glu Ala Gly Asn Glu Phe Val Gln His Asn Thr
530 535 540

Arg Gln Leu Ser Arg Val Tyr Pro Ser Gly Leu Arg Thr Gly Ser Ser
545 550 555 560

Ile Tyr Asn Pro Gln Gly Tyr
565

<210> 9

<211> 1384

<212> DNA

<213> Homo sapiens

<400> 9

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gaaaaaataa atgcagatgt tggaccatgt tggaaacctt gtcaagacag tggattgtct 180

cacacagaat ggaaatgtgg cttctgattc tgggtggcgta tatgttccag agaaatgtga 240

attcagtaca tatgccaaact aaagctgtgg acccagaagc attcatgaat attagtga 300

tcaccaaca tcaaggctat ccctgtgagg aatatgaagt cgcaactgaa gatgggtata 360
 tcctttctgt taacaggatt cctcgaggcc tagtgcaacc taagaagaca gggtccaggc 420
 ctgtggtgtt actgcagcat ggcctagttg gaggtgctag caactggatt tccaacctgc 480
 ccaacaatag cctgggcttc attctggcag atgctggttt tgacgtgtgg atggggaaca 540
 gcaggggaaa cgctgtgtct cgaaaacaca agacactctc catagaccaa gatgagttct 600
 gggctttcag ttatgatgag atggctaggt ttgaccttcc tgcagtgata aactttattt 660
 tgcagaaaac gggccaggaa aagatctatt atgtcggcta ttcacagggc accaccatgg 720
 gctttattgc attttccacc atgccagagc tggctcagaa aatcaaaatg tattttgctt 780
 tagcaccat agccactgtt aagcatgcaa aaagccccgg gaccaaattt ttgttgctgc 840
 cagatatgat gatcaaggga ttgtttggca aaaaagaatt tctgtatcag accagatttc 900
 tcagacaact tgttatttac ctttgtggcc aggtgattct tgatcagatt ttagtaata 960
 tcatgttact tctgggtgga ttcaacacca acaatatgaa catgagccga gcaagtgtat 1020
 atgtgocca cactcttgcg ggaacatctg tgcaaaatat tctacactgg agccaggcag 1080
 tgaattctgg tgaactccgg gcatttgact gggggagtga gacaaaaat ctggaaaaat 1140
 gcaatcagcc aactcctgta aggtacagag tcagagatat gacggtcctt acagcaatgt 1200
 ggacaggagg tcaggactgg ctttcaaatc cagaagacgt gaaaatgctg ctctctgagg 1260
 tgaccaacct catctaccat aagaatattc ctgaatgggc tcatgtggat ttcattctggg 1320
 gtttgatgc tctcaccgt atgtacaatg aaatcatcca tctgatgcag caggaggaga 1380
 ccat 1384

<210> 10
 <211> 1915
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (180)..(1046)

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 cagtagcccg gcggcccagg gcaatccgac cacatttcac tctcaccgct gtaggaatcc 120
 agatgcaggc caagtacagc agcagcaggg acatgctgga tgatgatggg gacaccacc 179
 atg agc ctg cat tct caa gcc tct gcc aca act cgg cat cca gag ccc 227
 Met Ser Leu His Ser Gln Ala Ser Ala Thr Arg His Pro Glu Pro
 1 5 10 15
 cgg cgc aca gag cac agg gct ccc tct tca acg tgg cga cca gtg gcc 275
 Arg Arg Thr Glu His Arg Ala Pro Ser Ser Thr Trp Arg Pro Val Ala
 20 25 30

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
2	2	1	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
3	3	2	1	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
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5	5	4	3	2	1	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80																				

tga ttcgccctct gcaactacaa atagcagagt gagccaggcg gtgccaaagc 1096
aagggctagt tgagacattg ggaaatggaa cataatcagg aaagactatc tctctgacta 1156
gtacaaaatg ggttctcgtg tttcctgttc aggatcacca gcatttctga gcttgggttt 1216
atgcacgtat ttaacagtca caagaagtct tatttacatg ccaccaacca acctcagaaa 1276
cccataatgt catctgcctt cttggcttag agataacttt tagctctctt tcttctcaat 1336
gtctaataatc acctccctgt tttcatgtct tccttacact tgggtggaata agaaactttt 1396
tgaagtagag gaataacatt gaggtaacat ccttttctct gacagtcaag tagtccatca 1456
gaaattggca gtcacttccc agattgtacc agcaaataca caaggaattc tttttgtttg 1516
tttcagttca tactagtccc ttccaatcc atcagtaaag accccatctg ccttgtccat 1576
gccgtttccc aacagggatg tcacttgata tgagaatctc aaatctcaat gccttataag 1636
cattccttcc tgtgtccatt aagactctga taattgtctc ccctccatag gaatttctcc 1696
caggaaagaa atatatcccc atctccgttt catatcagaa ctaccgtccc cgatattccc 1756
ttcagagaga ttaaagacca gaaaaaagg gggctttttt tttgcacctg taatagtttc 1816
cggtcctttt ttttttctt gaccctttt ttttccctt cggggggtgga ggggttatta 1876
taattaaagg gaataccggg gaaaaaaaaa aaaaagggg 1915

<210> 11
<211> 288
<212> PRT
<213> Homo sapiens

<400> 11

Met Ser Leu His Ser Gln Ala Ser Ala Thr Thr Arg His Pro Glu Pro
1 5 10 15

Arg Arg Thr Glu His Arg Ala Pro Ser Ser Thr Trp Arg Pro Val Ala
20 25 30

Leu Thr Leu Leu Thr Leu Cys Leu Val Leu Leu Ile Gly Leu Ala Ala
35 40 45

Leu Gly Leu Leu Phe Phe Gln Tyr Tyr Gln Leu Ser Asn Thr Gly Gln
50 55 60

Asp Thr Ile Ser Gln Met Glu Glu Arg Leu Gly Asn Thr Ser Gln Glu
65 70 75 80

Leu Gln Ser Leu Gln Val Gln Asn Ile Lys Leu Ala Gly Ser Leu Gln
85 90 95

His Val Ala Glu Lys Leu Cys Arg Glu Leu Tyr Asn Lys Ala Gly Gly

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<210> 12
<211> 2420
<212> DNA
<213> Homo sapiens
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<220>
<221>   CDS
<222>   (200)..(2395)
<223>   Xaa = Unknown or other
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gaagtcctag gactaatctc caggaccagc actcttctcc cagcccttag ggtcctgctc      180

ggccaaggcc ttccctgcc atg cga cct gtc agt gtc tgg cag tgg agc ccc      232
          Met Arg Pro Val Ser Val Trp Gln Trp Ser Pro
                1             5             10

tgg ggg ctg ctg ctg tgc ctg ctg tgc agt tgc tgc ttg ggg tct ccg      280
Trp Gly Leu Leu Leu Cys Leu Leu Cys Ser Ser Cys Leu Gly Ser Pro
                15             20             25

tcc cct tcc acg ggc cct gag aag aag gcc ggg agc cag ggg ctt cgg      328
Ser Pro Ser Thr Gly Pro Glu Lys Lys Ala Gly Ser Gln Gly Leu Arg
                30             35             40

ttc cgg ctg gct ggc ttc ccc agg aag ccc tac gag ggc cgc gtg gag      376
Phe Arg Leu Ala Gly Phe Pro Arg Lys Pro Tyr Glu Gly Arg Val Glu
                45             50             55

ata cag cga gct ggt gaa tgg ggc acc atc tgc gat gat gac ttc acg      424
Ile Gln Arg Ala Gly Glu Trp Gly Thr Ile Cys Asp Asp Asp Phe Thr
        60             65             70             75

ctg cag gct gcc cac atc ctg tgc cgg gag ctg ggc ttc aca gag gcc      472
Leu Gln Ala Ala His Ile Leu Cys Arg Glu Leu Gly Phe Thr Glu Ala
                80             85             90

aca ggc tgg acc cac agt gcc aaa tat ggc cct gga aca ggc cgc atc      520
Thr Gly Trp Thr His Ser Ala Lys Tyr Gly Pro Gly Thr Gly Arg Ile
                95             100             105

tgg ctg gac aac ttg agc tgc agt ggg acc gag cag agt gtg act gaa      568
Trp Leu Asp Asn Leu Ser Cys Ser Gly Thr Glu Gln Ser Val Thr Glu
                110             115             120

tgt gcc tcc cgg ggc tgg ggg aac agt gac tgt acg cac gat gag gat      616
Cys Ala Ser Arg Gly Trp Gly Asn Ser Asp Cys Thr His Asp Glu Asp
                125             130             135

gct ggg gtc atc tgc aaa gac cag cgc ctg cct ggc ttc tgc gac tcc      664
Ala Gly Val Ile Cys Lys Asp Gln Arg Leu Pro Gly Phe Ser Asp Ser
        140             145             150             155

aat gtc att gag gta gag cat cac ctg caa gtg gag gag gtg cga att      712
Asn Val Ile Glu Val Glu His His Leu Gln Val Glu Glu Val Arg Ile
                160             165             170

cga ccc gcc gtt ggg tgg ggc aga cga ccc ctg ccc gtg acg gag ggg      760
Arg Pro Ala Val Gly Trp Gly Arg Arg Pro Leu Pro Val Thr Glu Gly
                175             180             185

ctg gtg gaa gtc agg ctt cct gac ggc tgg tgc caa gtg tgc gac aaa      808
Leu Val Glu Val Arg Leu Pro Asp Gly Trp Ser Gln Val Cys Asp Lys
                190             195             200

ggc tgg agc gcc cac aac agc cac gtg gtc tgc ggg atg ctg ggc ttc      856
Gly Trp Ser Ala His Asn Ser His Val Val Cys Gly Met Leu Gly Phe
                205             210             215

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ccc agc gaa aag agg gtc aac gcg gcc ttc tac agg ctg cta gcc caa Pro Ser Glu Lys Arg Val Asn Ala Ala Phe Tyr Arg Leu Leu Ala Gln 220 225 230 235	904
cgg cag caa cac tcc ttt ggt ctg cat ggg gtg gcg tgc gtg ggc acg Arg Gln Gln His Ser Phe Gly Leu His Gly Val Ala Cys Val Gly Thr 240 245 250	952
gag gcc cac ctg tcc ctg tgt tcc ctg gag ttc tat cgt gcc aat gac Glu Ala His Leu Ser Leu Cys Ser Leu Glu Phe Tyr Arg Ala Asn Asp 255 260 265	1000
acc gcc agg tgc cct ggg ggg ggc cct gca gtg gtg agc tgt gtg cca Thr Ala Arg Cys Pro Gly Gly Gly Pro Ala Val Val Ser Cys Val Pro 270 275 280	1048
ggc cct gtc tac gcg gca tcc agt ggc cag aag aag caa caa cag tcg Gly Pro Val Tyr Ala Ala Ser Ser Gly Gln Lys Lys Gln Gln Gln Ser 285 290 295	1096
aag cct cag ggg gag gtc cgt gtc cgt cta aag ggc ggc gcc cac cct Lys Pro Gln Gly Glu Val Arg Val Arg Leu Lys Gly Gly Ala His Pro 300 305 310 315	1144
gga gag ggc cgg gta gaa gtc ctg aag gcc agc aca tgg ggc aca gtc Gly Glu Gly Arg Val Glu Val Leu Lys Ala Ser Thr Trp Gly Thr Val 320 325 330	1192
tgt tac cgc aag tgg gac ctg cat gca gcc agc gtg gtg tgt cgg gag Cys Tyr Arg Lys Trp Asp Leu His Ala Ala Ser Val Val Cys Arg Glu 335 340 345	1240
ctg ggc ttc ggg agt gct cga gaa gct ctg agt ggc gct cgc atg ggg Leu Gly Phe Gly Ser Ala Arg Glu Ala Leu Ser Gly Ala Arg Met Gly 350 355 360	1288
cag ggc atg ggt gct atc cac ctg agt gaa gtt cgc tgc tct gga cag Gln Gly Met Gly Ala Ile His Leu Ser Glu Val Arg Cys Ser Gly Gln 365 370 375	1336
gag ctg tcc ctg tgg aag tgc ccc cac aag aac atc aca gct gag gat Glu Leu Ser Leu Trp Lys Cys Pro His Lys Asn Ile Thr Ala Glu Asp 380 385 390 395	1384
tgt tca cat agc cag gat gcc ggg gtc cgg tgc aac cta cct tac act Cys Ser His Ser Gln Asp Ala Gly Val Arg Cys Asn Leu Pro Tyr Thr 400 405 410	1432
ggg gca gag acc agg gtc atc cat tct gtg tca cta cag atc cga ctg Gly Ala Glu Thr Arg Val Ile His Ser Val Ser Leu Gln Ile Arg Leu 415 420 425	1480
agt ggg ggc cgc agc caa cat gag ggg cga gtc gag gtg caa ata ggg Ser Gly Gly Arg Ser Gln His Glu Gly Arg Val Glu Val Gln Ile Gly 430 435 440	1528
gga cct ggg ccc ctt cgc tgg ggc ctg atc tgt ggg gat gac tgg ggg Gly Pro Gly Pro Leu Arg Trp Gly Leu Ile Cys Gly Asp Asp Trp Gly 445 450 455	1576
acc ctg gag gcc atg gtg gcc tgt agg caa ctg ggt ctg ggc tac gcc Thr Leu Glu Ala Met Val Ala Cys Arg Gln Gly Leu Gly Tyr Ala 460 465 470 475	1624

aac cac ggc ctg cag gag acc tgg tac tgg gac tct ggg aat ata aca	1672
Asn His Gly Leu Gln Glu Thr Trp Tyr Trp Asp Ser Gly Asn Ile Thr	
480 485 490	
gag gtg gtg atg agt gga gtg cgc tgc aca ggg act gag ctg tcc ctg	1720
Glu Val Val Met Ser Gly Val Arg Cys Thr Gly Thr Glu Leu Ser Leu	
495 500 505	
gat cag tgt gcc cat cat ggc acc cac atc acc tgc aag agg aca ggg	1768
Asp Gln Cys Ala His His Gly Thr His Ile Thr Cys Lys Arg Thr Gly	
510 515 520	
acc cgc ttc act gct gga gtc atc tgt tct gag gca tca gat ctg ttg	1816
Thr Arg Phe Thr Ala Gly Val Ile Cys Ser Glu Ala Ser Asp Leu Leu	
525 530 535	
ctg cac tca gca ctg gtg cag gag acc gcc tac atc gaa gac cgg ccc	1864
Leu His Ser Ala Leu Val Gln Glu Thr Ala Tyr Ile Glu Asp Arg Pro	
540 545 550 555	
ctg cat atg ttg tac tgt gct gcg gaa gag aac tgc ctg gcc agc tca	1912
Leu His Met Leu Tyr Cys Ala Ala Glu Glu Asn Cys Leu Ala Ser Ser	
560 565 570	
gcc cgc tca gcc aac tgg ccc tat ggt cac cgg cgt ctg ctc cga ttc	1960
Ala Arg Ser Ala Asn Trp Pro Tyr Gly His Arg Arg Leu Leu Arg Phe	
575 580 585	
tgc tcc cag atc cac aac ctg gga cga gct gac ttc agg ccc aag gct	2008
Cys Ser Gln Ile His Asn Leu Gly Arg Ala Asp Phe Arg Pro Lys Ala	
590 595 600	
ggg cgc cac tcc tgg gtg tgg cac gag tgc cat ggg cat tac cac agc	2056
Gly Arg His Ser Trp Val Trp His Glu Cys His Gly His Tyr His Ser	
605 610 615	
acg gac ttc ttc act cac tat gat atc ctc acc cca nat ggc acc aag	2104
Thr Asp Phe Phe Thr His Tyr Asp Ile Leu Thr Pro Xaa Gly Thr Lys	
620 625 630 635	
gtg gct gag ggc cac aaa gct agt ttc tgt ctc gaa gac act gag tgt	2152
Val Ala Glu Gly His Lys Ala Ser Phe Cys Leu Glu Asp Thr Glu Cys	
640 645 650	
cag gag gat gtc tcc aag cgg tat gag tgt gcc aac ttt gga gag caa	2200
Gln Glu Asp Val Ser Lys Arg Tyr Glu Cys Ala Asn Phe Gly Glu Gln	
655 660 665	
ggc atc act gtg ggd tgc tgg gat ctc tac cgg cat gac att gac tgt	2248
Gly Ile Thr Val Xaa Cys Trp Asp Leu Tyr Arg His Asp Ile Asp Cys	
670 675 680	
cag tgg att gac atc acg gat gtg aag cca gga aac tac att ctc cag	2296
Gln Trp Ile Asp Ile Thr Asp Val Lys Pro Gly Asn Tyr Ile Leu Gln	
685 690 695	
gtt gtc atc aac cca aac ttt gaa gta gca gag agb gac ttt acc aac	2344
Val Val Ile Asn Pro Asn Phe Glu Val Ala Glu Xaa Asp Phe Thr Asn	
700 705 710 715	
aat gca atg aaa tgt aac tgc aaa tat gat gga cat aga atc tgg gtg	2392
Asn Ala Met Lys Cys Asn Cys Lys Tyr Asp Gly His Arg Ile Trp Val	
720 725 730	

cac macttgccac attggtgatg ccttc
His

<210> 13
<211> 732
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> n = a or c or g or t

<400> 13

Met Arg Pro Val Ser Val Trp Gln Trp Ser Pro Trp Gly Leu Leu Leu
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Cys Leu Leu Cys Ser Ser Cys Leu Gly Ser Pro Ser Pro Ser Thr Gly
20 25 30

Pro Glu Lys Lys Ala Gly Ser Gln Gly Leu Arg Phe Arg Leu Ala Gly
35 40 45

Phe Pro Arg Lys Pro Tyr Glu Gly Arg Val Glu Ile Gln Arg Ala Gly
50 55 60

Glu Trp Gly Thr Ile Cys Asp Asp Asp Phe Thr Leu Gln Ala Ala His
65 70 75 80

Ile Leu Cys Arg Glu Leu Gly Phe Thr Glu Ala Thr Gly Trp Thr His
85 90 95

Ser Ala Lys Tyr Gly Pro Gly Thr Gly Arg Ile Trp Leu Asp Asn Leu
100 105 110

Ser Cys Ser Gly Thr Glu Gln Ser Val Thr Glu Cys Ala Ser Arg Gly
115 120 125

Trp Gly Asn Ser Asp Cys Thr His Asp Glu Asp Ala Gly Val Ile Cys
130 135 140

Lys Asp Gln Arg Leu Pro Gly Phe Ser Asp Ser Asn Val Ile Glu Val
145 150 155 160

Glu His His Leu Gln Val Glu Glu Val Arg Ile Arg Pro Ala Val Gly
165 170 175

Trp Gly Arg Arg Pro Leu Pro Val Thr Glu Gly Leu Val Glu Val Arg
180 185 190

Leu Pro Asp Gly Trp Ser Gln Val Cys Asp Lys Gly Trp Ser Ala His
195 200 205

Asn Ser His Val Val Cys Gly Met Leu Gly Phe Pro Ser Glu Lys Arg
210 215 220

Val Asn Ala Ala Phe Tyr Arg Leu Leu Ala Gln Arg Gln Gln His Ser
225 230 235 240

Phe Gly Leu His Gly Val Ala Cys Val Gly Thr Glu Ala His Leu Ser
245 250 255

Leu Cys Ser Leu Glu Phe Tyr Arg Ala Asn Asp Thr Ala Arg Cys Pro
260 265 270

Gly Gly Gly Pro Ala Val Val Ser Cys Val Pro Gly Pro Val Tyr Ala
275 280 285

Ala Ser Ser Gly Gln Lys Lys Gln Gln Gln Ser Lys Pro Gln Gly Glu
290 295 300

Val Arg Val Arg Leu Lys Gly Gly Ala His Pro Gly Glu Gly Arg Val
305 310 315 320

Glu Val Leu Lys Ala Ser Thr Trp Gly Thr Val Cys Tyr Arg Lys Trp
325 330 335

Asp Leu His Ala Ala Ser Val Val Cys Arg Glu Leu Gly Phe Gly Ser
340 345 350

Ala Arg Glu Ala Leu Ser Gly Ala Arg Met Gly Gln Gly Met Gly Ala
355 360 365

Ile His Leu Ser Glu Val Arg Cys Ser Gly Gln Glu Leu Ser Leu Trp
370 375 380

Lys Cys Pro His Lys Asn Ile Thr Ala Glu Asp Cys Ser His Ser Gln
385 390 395 400

Asp Ala Gly Val Arg Cys Asn Leu Pro Tyr Thr Gly Ala Glu Thr Arg
405 410 415

Val Ile His Ser Val Ser Leu Gln Ile Arg Leu Ser Gly Gly Arg Ser
420 425 430

Gln His Glu Gly Arg Val Glu Val Gln Ile Gly Gly Pro Gly Pro Leu
435 440 445

195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400 405 410 415 420 425 430 435 440 445

Arg Trp Gly Leu Ile Cys Gly Asp Asp Trp Gly Thr Leu Glu Ala Met
450 455 460

Val Ala Cys Arg Gln Leu Gly Leu Gly Tyr Ala Asn His Gly Leu Gln
465 470 475 480

Glu Thr Trp Tyr Trp Asp Ser Gly Asn Ile Thr Glu Val Val Met Ser
485 490 495

Gly Val Arg Cys Thr Gly Thr Glu Leu Ser Leu Asp Gln Cys Ala His
500 505 510

His Gly Thr His Ile Thr Cys Lys Arg Thr Gly Thr Arg Phe Thr Ala
515 520 525

Gly Val Ile Cys Ser Glu Ala Ser Asp Leu Leu Leu His Ser Ala Leu
530 535 540

Val Gln Glu Thr Ala Tyr Ile Glu Asp Arg Pro Leu His Met Leu Tyr
545 550 555 560

Cys Ala Ala Glu Glu Asn Cys Leu Ala Ser Ser Ala Arg Ser Ala Asn
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Trp Pro Tyr Gly His Arg Arg Leu Leu Arg Phe Cys Ser Gln Ile His
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Asn Leu Gly Arg Ala Asp Phe Arg Pro Lys Ala Gly Arg His Ser Trp
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Val Trp His Glu Cys His Gly His Tyr His Ser Thr Asp Phe Phe Thr
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His Tyr Asp Ile Leu Thr Pro Xaa Gly Thr Lys Val Ala Glu Gly His
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Lys Ala Ser Phe Cys Leu Glu Asp Thr Glu Cys Gln Glu Asp Val Ser
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Cys Trp Asp Leu Tyr Arg His Asp Ile Asp Cys Gln Trp Ile Asp Ile
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Thr Asp Val Lys Pro Gly Asn Tyr Ile Leu Gln Val Val Ile Asn Pro
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Protein Accession

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Phe Leu Leu Ala Leu Leu Thr Leu Ser Gly Leu Leu Pro Ile Ala Arg
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Val Leu Thr Val Gly Ala Asp Arg Asp Gln Gln Leu Cys Asp Pro Gly
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Glu Phe Leu Cys His Asp His Val Thr Cys Val Ser Gln Ser Trp Leu
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Cys Asp Gly Asp Pro Asp Cys Pro Asp Asp Ser Asp Glu Ser Leu Asp
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acc tgt ccc gag gag gta gaa atc aag tgc ccc ttg aat cac att gct 508
Thr Cys Pro Glu Glu Val Glu Ile Lys Cys Pro Leu Asn His Ile Ala
105 110 115 120
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Cys Leu Gly Thr Asn Lys Cys Val His Leu Ser Gln Leu Cys Asn Gly
125 130 135
gtc ttg gac tgc cca gat ggg tat gac gaa gga gta cat tgt cag gaa 604
Val Leu Asp Cys Pro Asp Gly Tyr Asp Glu Gly Val His Cys Gln Glu
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Lys	Ile	Glu	Pro	Thr	Asp	Arg	Pro	Arg	Ile	Leu	Leu	Ile	Ala	Asn	Phe	
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Ile	Asn	Ile	Leu	Gln	Ser	Phe	His	Asn	Val	Gln	Gln	Met	Ala	Ile	Asp	
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Trp	Leu	Thr	Arg	Asn	Leu	Tyr	Phe	Val	Asp	His	Val	Gly	Asp	Arg	Ile	
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Pro Ala Ala Leu Ala Leu Asp Leu Val Asn Lys Leu Val Tyr Trp Val	
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Asp Leu Tyr Leu Asp Tyr Val Gly Val Val Asp Tyr Gln Gly Lys Asn	
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Thr Val Phe Glu Asp Tyr Leu Tyr Ala Thr Asn Ser Asp Asn Tyr Asn	
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Ile Val Arg Ile Asn Arg Phe Asn Gly Thr Asp Ile His Ser Leu Ile	
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Gly Gly Cys Ser His Ile Cys Leu Leu Ser Ser Ser Tyr Lys Thr Arg	
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Cys Lys Arg Pro Lys Asn Glu Leu Phe Leu Phe Tyr Gly Lys Gly Arg	
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Tyr Met Ile Pro Ile Glu Asn Leu Val Asn Pro Arg Ala Leu Asp Phe	
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His Ala Glu Thr Asn Tyr Ile Tyr Phe Ala Asp Thr Thr Ser Phe Leu	
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260 265 270

His Thr Leu Asp Phe Ile Tyr Asn Glu Asp Val Ile Cys Trp Ile Glu
275 280 285

Ser Arg Glu Ser Ser Asn Gln Leu Lys Cys Ile Gln Ile Thr Lys Ala
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Gly Gly Leu Thr Asp Glu Trp Thr Ile Asn Ile Leu Gln Ser Phe His
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Asn Val Gln Gln Met Ala Ile Asp Trp Leu Thr Arg Asn Leu Tyr Phe
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Val Asp His Val Gly Asp Arg Ile Phe Val Cys Asn Ser Asn Gly Ser
340 345 350

Val Cys Val Thr Leu Ile Asp Leu Glu Leu His Asn Pro Lys Ala Ile
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Ala Val Asp Pro Ile Ala Gly Lys Leu Phe Phe Thr Asp Tyr Gly Asn
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Val Ala Lys Val Glu Arg Cys Asp Met Asp Gly Met Asn Arg Thr Arg
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Ile Ile Asp Ser Lys Thr Glu Gln Pro Ala Ala Leu Ala Leu Asp Leu
405 410 415

Val Asn Lys Leu Val Tyr Trp Val Asp Leu Tyr Leu Asp Tyr Val Gly
420 425 430

Val Val Asp Tyr Gln Gly Lys Asn Arg His Thr Val Ile Gln Gly Arg
435 440 445

Gln Val Arg His Leu Tyr Gly Ile Thr Val Phe Glu Asp Tyr Leu Tyr
450 455 460

Ala Thr Asn Ser Asp Asn Tyr Asn Ile Val Arg Ile Asn Arg Phe Asn
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Gly Thr Asp Ile His Ser Leu Ile Lys Ile Glu Asn Ala Trp Gly Ile
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LEU-1000

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Thr	Ser	Asp	Glu	Ala	Trp	Lys	Arg	Phe	Val	Arg	Val	Ala	Glu	Leu	Pro	
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Ser Gly Val Leu Val Val Leu Asp Val Val Asn Leu Val Gln Asp Ser
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Leu Asp Leu His Lys Gly Ala Lys Ser Glu Ser Ala Glu Ser Leu Arg
310                      315                      320                      325

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Gln Trp Ala Gln Glu Leu Glu Glu Asn Leu Asn Glu Leu Thr His Ile
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Val Ala Glu Leu Pro Arg Glu Glu Ala Asp Ala Leu Tyr Glu Ala Leu
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Lys Asn Leu Thr Pro Tyr Val Ala Ile Glu Asp Lys Asp Met Gln Gln
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Lys Glu Gln Gln Phe Arg Glu Trp Phe Leu Lys Glu Phe Pro Gln Ile
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180 185 190

Tyr Thr Arg Ser Ala Glu Leu Thr Ala Ser Arg Leu Thr Ala Thr Ser
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Thr Asp Gln Leu Glu Ala Leu Arg Asp Ile Leu Arg Asp Ile Thr Pro
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Asn Val Leu Ser Phe Ala Leu Asp Phe Asp Glu Ala Thr Lys Met Ile
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Ala Asn Asp Val His Thr Leu Arg Arg Ser Lys Ala Thr Val Gly Arg
245 250 255

Pro Leu Ile Ala Trp Arg Tyr Val Pro Ile Asn Val Val Glu Thr Leu
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Arg Thr Arg Gly Ala Pro Thr Arg Ile Val Arg Lys Val Ala Arg Asn
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Leu Gly Lys Ala Thr Ser Gly Val Leu Val Val Leu Asp Val Val Asn
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Leu Val Gln Asp Ser Leu Asp Leu His Lys Gly Ala Lys Ser Glu Ser
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Leu Thr Thr Asp Gln Asp Leu Leu Leu Met Gln Glu Gly Met Pro Met	
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His Asp Ser Glu Leu Leu Arg Ser Leu Ala Glu Glu Leu Pro Leu Glu	
75 80 85	
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Gln Gly Phe Thr Ile Val Phe His Gly Arg Arg Ser Asn Leu Asp Leu	
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atg gcc aac agt gtt gag gag gcc cag ata tgg atg cga ggg ctc cag	510
Met Ala Asn Ser Val Glu Glu Ala Gln Ile Trp Met Arg Gly Leu Gln	
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Gln Trp Leu Ser Asp Trp Phe Gln Arg Gly Asp Lys Asn Gln Asp Gly	
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aag atg agt ttc caa gaa gtt cag cgg tta ttg cac cta atg aat gtg	654
Lys Met Ser Phe Gln Glu Val Gln Arg Leu Leu His Leu Met Asn Val	
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gaa atg gac caa gaa tat gcc ttc agt ctt ttt cag gca gca gac acg	702
Glu Met Asp Gln Glu Tyr Ala Phe Ser Leu Phe Gln Ala Ala Asp Thr	
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Ser Gln Ser Gly Thr Leu Glu Gly Glu Glu Phe Val Gln Phe Tyr Lys	
185 190 195 200	
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Ala Leu Thr Lys Arg Ala Glu Val Gln Glu Leu Phe Glu Ser Phe Ser	
205 210 215	
gct gat ggg cag aag ctg act ctg ctg gaa ttt ttg gat ttc ctc caa	846
Ala Asp Gly Gln Lys Leu Thr Leu Leu Glu Phe Leu Asp Phe Leu Gln	
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120 174 222 270 318 366 414 462 510 558 606 654 702 750 798 846 894

Glu Glu Gln Lys Glu Arg Asp Cys Thr Ser Glu Leu Ala Leu Glu Leu
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Ile Asp Arg Tyr Glu Pro Ser Asp Ser Gly Lys Leu Arg His Val Leu
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Ser Met Asp Gly Phe Leu Ser Tyr Leu Cys Ser Lys Asp Gly Asp Ile
265 270 275 280

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285 290 295

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Asn His Tyr Phe Ile Cys Ser Ser His Asn Thr Tyr Leu Val Gly Asp
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Gln Leu Cys Gly Gln Ser Ser Val Glu Gly Tyr Ile Arg Cys Ser Gly
315 320 325

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Gly Arg Glu Gly Val Gln Leu Met Arg Gly Thr Met
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aaccctatgg gtcaatggaa cttctctttc acaagctatg aaactctcct ggaactcaga 1360

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Lys Lys Leu Arg Tyr Phe Arg Leu Gln Asn Asp Gly Met Thr Val Trp
35 40 45

His Ala Arg Gln Ala Arg Gly Ser Ala Lys Pro Ser Phe Ser Ile Ser
50 55 60

CCDS=CCDS

Asp Val Glu Thr Ile Arg Asn Gly His Asp Ser Glu Leu Leu Arg Ser
65 70 75 80

Leu Ala Glu Glu Leu Pro Leu Glu Gln Gly Phe Thr Ile Val Phe His
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Gly Arg Arg Ser Asn Leu Asp Leu Met Ala Asn Ser Val Glu Glu Ala
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Gln Ile Trp Met Arg Gly Leu Gln Leu Leu Val Asp Leu Val Thr Ser
115 120 125

Met Asp His Gln Glu Arg Leu Asp Gln Trp Leu Ser Asp Trp Phe Gln
130 135 140

Arg Gly Asp Lys Asn Gln Asp Gly Lys Met Ser Phe Gln Glu Val Gln
145 150 155 160

Arg Leu Leu His Leu Met Asn Val Glu Met Asp Gln Glu Tyr Ala Phe
165 170 175

Ser Leu Phe Gln Ala Ala Asp Thr Ser Gln Ser Gly Thr Leu Glu Gly
180 185 190

Glu Glu Phe Val Gln Phe Tyr Lys Ala Leu Thr Lys Arg Ala Glu Val
195 200 205

Gln Glu Leu Phe Glu Ser Phe Ser Ala Asp Gly Gln Lys Leu Thr Leu
210 215 220

Leu Glu Phe Leu Asp Phe Leu Gln Glu Glu Gln Lys Glu Arg Asp Cys
225 230 235 240

Thr Ser Glu Leu Ala Leu Glu Leu Ile Asp Arg Tyr Glu Pro Ser Asp
245 250 255

Ser Gly Lys Leu Arg His Val Leu Ser Met Asp Gly Phe Leu Ser Tyr
260 265 270

Leu Cys Ser Lys Asp Gly Asp Ile Phe Asn Pro Ala Cys Leu Pro Ile
275 280 285

Tyr Gln Asp Met Thr Gln Pro Leu Asn His Tyr Phe Ile Cys Ser Ser
290 295 300

His Asn Thr Tyr Leu Val Gly Asp Gln Leu Cys Gly Gln Ser Ser Val
305 310 315 320

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Arg Gly Thr Met
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gaaaaataaa atgcagatgt tggaccatgt tggaaacctt gtcaagacag tggattgtct 180
cacacaga atg gaa atg tgg ctt ctg att ctg gtg gcg tat atg ttc cag 230
Met Glu Met Trp Leu Leu Ile Leu Val Ala Tyr Met Phe Gln
1 5 10
aga aat gtg aat tca gta cat atg cca act aaa gct gtg gac cca gaa 278
Arg Asn Val Asn Ser Val His Met Pro Thr Lys Ala Val Asp Pro Glu
15 20 25 30
gca ttc atg aat att agt gaa atc atc caa cat caa ggc tat ccc tgt 326
Ala Phe Met Asn Ile Ser Glu Ile Ile Gln His Gln Gly Tyr Pro Cys
35 40 45
gag gaa tat gaa gtc gca act gaa gat ggg tat atc ctt tct gtt aac 374
Glu Glu Tyr Glu Val Ala Thr Glu Asp Gly Tyr Ile Leu Ser Val Asn
50 55 60
agg att cct cga ggc cta gtg caa cct aag aag aca ggt tcc agg cct 422
Arg Ile Pro Arg Gly Leu Val Gln Pro Lys Lys Thr Gly Ser Arg Pro
65 70 75
gtg gtg tta ctg cag cat ggc cta gtt gga ggt gct agc aac tgg att 470
Val Val Leu Leu Gln His Gly Leu Val Gly Gly Ala Ser Asn Trp Ile
80 85 90
tcc aac ctg ccc aac aat agc ctg ggc ttc att ctg gca gat gct ggt 518
Ser Asn Leu Pro Asn Asn Ser Leu Gly Phe Ile Leu Ala Asp Ala Gly
95 100 105 110
ttt gac gtg tgg atg ggg aac agc agg gga aac gcc tgg tct cga aaa 566
Phe Asp Val Trp Met Gly Asn Ser Arg Gly Asn Ala Trp Ser Arg Lys
115 120 125
cac aag aca ctc tcc ata gac caa gat gag ttc tgg gct ttc agt tat 614
His Lys Thr Leu Ser Ile Asp Gln Asp Glu Phe Trp Ala Phe Ser Tyr
130 135 140
gat gag atg gct agg ttt gac ctt cct gca gtg ata aac ttt att ttg 662
Asp Glu Met Ala Arg Phe Asp Leu Pro Ala Val Ile Asn Phe Ile Leu
145 150 155

cag aaa acg ggc cag gaa aag atc tat tat gtc ggc tat tca cag ggc Gln Lys Thr Gly Gln Glu Lys Ile Tyr Tyr Val Gly Tyr Ser Gln Gly 160 165 170	710
acc acc atg ggc ttt att gca ttt tcc acc atg cca gag ctg gct cag Thr Thr Met Gly Phe Ile Ala Phe Ser Thr Met Pro Glu Leu Ala Gln 175 180 185 190	758
aaa atc aaa atg tat ttt gct tta gca ccc ata gcc act gtt aag cat Lys Ile Lys Met Tyr Phe Ala Leu Ala Pro Ile Ala Thr Val Lys His 195 200 205	806
gca aaa agc ccc ggg acc aaa ttt ttg ttg ctg cca gat atg atg atc Ala Lys Ser Pro Gly Thr Lys Phe Leu Leu Leu Pro Asp Met Met Ile 210 215 220	854
aag gga ttg ttt ggc aaa aaa gaa ttt ctg tat cag acc aga ttt ctc Lys Gly Leu Phe Gly Lys Lys Glu Phe Leu Tyr Gln Thr Arg Phe Leu 225 230 235	902
aga caa ctt gtt att tac ctt tgt ggc cag gtg att ctt gat cag att Arg Gln Leu Val Ile Tyr Leu Cys Gly Gln Val Ile Leu Asp Gln Ile 240 245 250	950
tgt agt aat atc atg tta ctt ctg ggt gga ttc aac acc aac aat atg Cys Ser Asn Ile Met Leu Leu Leu Gly Gly Phe Asn Thr Asn Asn Met 255 260 265 270	998
aac atg agc cga gca agt gta tat gct gcc cac act ctt gct gga aca Asn Met Ser Arg Ala Ser Val Tyr Ala Ala His Thr Leu Ala Gly Thr 275 280 285	1046
tct gtg caa aat att cta cac tgg agc cag gca gtg aat tct ggt gaa Ser Val Gln Asn Ile Leu His Trp Ser Gln Ala Val Asn Ser Gly Glu 290 295 300	1094
ctc cgg gca ttt gac tgg ggg agt gag acc aaa aat ctg gaa aaa tgc Leu Arg Ala Phe Asp Trp Gly Ser Glu Thr Lys Asn Leu Glu Lys Cys 305 310 315	1142
aat cag cca act cct gta agg tac aga gtc aga gat atg acg gtc cct Asn Gln Pro Thr Pro Val Arg Tyr Arg Val Arg Asp Met Thr Val Pro 320 325 330	1190
aca gca atg tgg aca gga ggt cag gac tgg ctt tca aat cca gaa gac Thr Ala Met Trp Thr Gly Gly Gln Asp Trp Leu Ser Asn Pro Glu Asp 335 340 345 350	1238
gtg aaa atg ctg ctc tct gag gtg acc aac ctc atc tac cat aag aat Val Lys Met Leu Leu Ser Glu Val Thr Asn Leu Ile Tyr His Lys Asn 355 360 365	1286
att cct gaa tgg gct cat gtg gat ttc atc tgg ggt ttg gat gct cct Ile Pro Glu Trp Ala His Val Asp Phe Ile Trp Gly Leu Asp Ala Pro 370 375 380	1334
cac cgt atg tac aat gaa atc atc cat ctg atg cag cag gag gag acc His Arg Met Tyr Asn Glu Ile Ile His Leu Met Gln Gln Glu Glu Thr 385 390 395	1382
aac ctt tcc cag gga cgg tgt gag gcc gta ttg tgaagcatct gacactgacg Asn Leu Ser Gln Gly Arg Cys Glu Ala Val Leu 400 405	1435

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atcttaggac aacctcctga gggatggggc taggacccat gaaggcagaa ttatggagag 1495
cagagaccta gtatacattt ttcagattcc ctgcacttgg cactaaatcc gacacttaca 1555
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tttttgagac actaaagtaa aatggcaaat tgggacagat attgagggtc ggagtctgtg 1795
gattattggt gactttgaca aaataagcta gacattttca ccttggtgcc acagagacat 1855
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tatggatgaa atctatgta agcattctca gaataaggcc aagttttata gttgcatctc 1975
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<210> 21
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<212> PRT
<213> Homo sapiens

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<400> 21

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Met Glu Met Trp Leu Leu Ile Leu Val Ala Tyr Met Phe Gln Arg Asn
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Val Asn Ser Val His Met Pro Thr Lys Ala Val Asp Pro Glu Ala Phe
          20          25          30

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Met Asn Ile Ser Glu Ile Ile Gln His Gln Gly Tyr Pro Cys Glu Glu
          35          40          45

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Tyr Glu Val Ala Thr Glu Asp Gly Tyr Ile Leu Ser Val Asn Arg Ile
          50          55          60

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Pro Arg Gly Leu Val Gln Pro Lys Lys Thr Gly Ser Arg Pro Val Val
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Leu Leu Gln His Gly Leu Val Gly Gly Ala Ser Asn Trp Ile Ser Asn
          85          90          95

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Leu Pro Asn Asn Ser Leu Gly Phe Ile Leu Ala Asp Ala Gly Phe Asp
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Val Trp Met Gly Asn Ser Arg Gly Asn Ala Trp Ser Arg Lys His Lys
          115          120          125

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Thr Leu Ser Ile Asp Gln Asp Glu Phe Trp Ala Phe Ser Tyr Asp Glu
          130          135          140

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Met Ala Arg Phe Asp Leu Pro Ala Val Ile Asn Phe Ile Leu Gln Lys
145 150 155 160

Thr Gly Gln Glu Lys Ile Tyr Tyr Val Gly Tyr Ser Gln Gly Thr Thr
165 170 175

Met Gly Phe Ile Ala Phe Ser Thr Met Pro Glu Leu Ala Gln Lys Ile
180 185 190

Lys Met Tyr Phe Ala Leu Ala Pro Ile Ala Thr Val Lys His Ala Lys
195 200 205

Ser Pro Gly Thr Lys Phe Leu Leu Leu Pro Asp Met Met Ile Lys Gly
210 215 220

Leu Phe Gly Lys Lys Glu Phe Leu Tyr Gln Thr Arg Phe Leu Arg Gln
225 230 235 240

Leu Val Ile Tyr Leu Cys Gly Gln Val Ile Leu Asp Gln Ile Cys Ser
245 250 255

Asn Ile Met Leu Leu Leu Gly Gly Phe Asn Thr Asn Asn Met Asn Met
260 265 270

Ser Arg Ala Ser Val Tyr Ala Ala His Thr Leu Ala Gly Thr Ser Val
275 280 285

Gln Asn Ile Leu His Trp Ser Gln Ala Val Asn Ser Gly Glu Leu Arg
290 295 300

Ala Phe Asp Trp Gly Ser Glu Thr Lys Asn Leu Glu Lys Cys Asn Gln
305 310 315 320

Pro Thr Pro Val Arg Tyr Arg Val Arg Asp Met Thr Val Pro Thr Ala
325 330 335

Met Trp Thr Gly Gly Gln Asp Trp Leu Ser Asn Pro Glu Asp Val Lys
340 345 350

Met Leu Leu Ser Glu Val Thr Asn Leu Ile Tyr His Lys Asn Ile Pro
355 360 365

Glu Trp Ala His Val Asp Phe Ile Trp Gly Leu Asp Ala Pro His Arg
370 375 380

Met Tyr Asn Glu Ile Ile His Leu Met Gln Gln Glu Glu Thr Asn Leu
385 390 395 400

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Ser Gln Gly Arg Cys Glu Ala Val Leu
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<222> (82)..(921)
<223> Xaa = Unknown or other

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Met Gln Ala Lys Tyr Ser Ser Thr Arg Asp
1 5 10
atg ctg gat gat gat ggg gac acc acc atg agc ctg cat tct caa gcc 159
Met Leu Asp Asp Asp Gly Asp Thr Thr Met Ser Leu His Ser Gln Ala
15 20 25
tct gcc aca act cgg cat cca gag ccc cgg cgc aca gag cac agg gct 207
Ser Ala Thr Thr Arg His Pro Glu Pro Arg Arg Thr Glu His Arg Ala
30 35 40
ccc tct tca acg tgg cga cca gtg gcc ctg acc ctg ctg act ttg tgc 255
Pro Ser Ser Thr Trp Arg Pro Val Ala Leu Thr Leu Leu Thr Leu Cys
45 50 55
ttg gtg ctg ctg ata ggg ctg gca gcc ctg ggg ctt ttg ttt ttt cag 303
Leu Val Leu Leu Ile Gly Leu Ala Ala Leu Gly Leu Leu Phe Phe Gln
60 65 70
tac tac cag ctg tcc aat act ggt caa gac acc att tct caa atg gaa 351
Tyr Tyr Gln Leu Ser Asn Thr Gly Gln Asp Thr Ile Ser Gln Met Glu
75 80 85 90
gaa aga tta gga aat acg tcc caa gag ttg caa tct ctt caa gtc cag 399
Glu Arg Leu Gly Asn Thr Ser Gln Glu Leu Gln Ser Leu Gln Val Gln
95 100 105
aat ata aag ctt gca gga agt ctg cag cat gtg gct gaa aaa ctg tgt 447
Asn Ile Lys Leu Ala Gly Ser Leu Gln His Val Ala Glu Lys Leu Cys
110 115 120
cgt gag ctg tat aac aaa gct gga gca cac agg tgc agc cct tgt aca 495
Arg Glu Leu Tyr Asn Lys Ala Gly Ala His Arg Cys Ser Pro Cys Thr
125 130 135
gaa caa tgg aaa tgg cat gga gac aat tgc tac cag ttc tat aaa gac 543
Glu Gln Trp Lys Trp His Gly Asp Asn Cys Tyr Gln Phe Tyr Lys Asp
140 145 150

agc	aaa	agt	tgg	gag	gac	tgt	aaa	tat	ttc	tgc	ctt	agt	gaa	aac	tct	591
Ser	Lys	Ser	Trp	Glu	Asp	Cys	Lys	Tyr	Phe	Cys	Leu	Ser	Glu	Asn	Ser	
155					160					165					170	
acc	atg	ctg	aag	ata	aac	aaa	caa	gaa	gac	ctg	gaa	ttt	gcc	gcg	tct	639
Thr	Met	Leu	Lys	Ile	Asn	Lys	Gln	Glu	Asp	Leu	Glu	Phe	Ala	Ala	Ser	
				175					180					185		
cag	agc	tac	tct	gag	ttt	ttc	tac	tct	tat	tgg	aca	ggg	ctt	ttg	cgc	687
Gln	Ser	Tyr	Ser	Glu	Phe	Phe	Tyr	Ser	Tyr	Trp	Thr	Gly	Leu	Leu	Arg	
			190					195					200			
cct	gac	agt	ggc	aag	gcc	tgg	ctg	tgg	atg	gat	gga	acc	cct	ttc	act	735
Pro	Asp	Ser	Gly	Lys	Ala	Trp	Leu	Trp	Met	Asp	Gly	Thr	Pro	Phe	Thr	
		205				210						215				
tct	gaa	ctg	ttc	cat	att	ata	ata	gat	gtc	acc	agc	cca	aga	agc	aga	783
Ser	Glu	Leu	Phe	His	Ile	Ile	Ile	Asp	Val	Thr	Ser	Pro	Arg	Ser	Arg	
	220				225						230					
gac	tgt	gtg	gcc	atc	ctt	aat	ggg	atg	atc	ttc	tca	aag	gac	tgc	aaa	831
Asp	Cys	Val	Ala	Ile	Leu	Asn	Gly	Met	Ile	Phe	Ser	Lys	Asp	Cys	Lys	
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gaa	ttg	aag	cgt	tgt	gtc	tgt	gag	aga	agg	gca	gga	atg	gtg	aag	cca	879
Glu	Leu	Lys	Arg	Cys	Val	Cys	Glu	Arg	Arg	Ala	Gly	Met	Val	Lys	Pro	
				255					260					265		
gag	agc	ctc	cat	gtc	ccc	cct	gaa	aca	tta	ggc	gaa	ggc	gac			921
Glu	Ser	Leu	His	Val	Pro	Pro	Glu	Thr	Leu	Gly	Glu	Gly	Asp			
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cccaacaggg	atgtcacttg	atatgagaat	ctcaaattct	aatgccttat	aagcatttct											1521
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<213> Homo sapiens

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Asp Thr Thr Met Ser Leu His Ser Gln Ala Ser Ala Thr Thr Arg His
20 25 30

Pro Glu Pro Arg Arg Thr Glu His Arg Ala Pro Ser Ser Thr Trp Arg
35 40 45

Pro Val Ala Leu Thr Leu Leu Thr Leu Cys Leu Val Leu Leu Ile Gly
50 55 60

Leu Ala Ala Leu Gly Leu Leu Phe Phe Gln Tyr Tyr Gln Leu Ser Asn
65 70 75 80

Thr Gly Gln Asp Thr Ile Ser Gln Met Glu Glu Arg Leu Gly Asn Thr
85 90 95

Ser Gln Glu Leu Gln Ser Leu Gln Val Gln Asn Ile Lys Leu Ala Gly
100 105 110

Ser Leu Gln His Val Ala Glu Lys Leu Cys Arg Glu Leu Tyr Asn Lys
115 120 125

Ala Gly Ala His Arg Cys Ser Pro Cys Thr Glu Gln Trp Lys Trp His
130 135 140

Gly Asp Asn Cys Tyr Gln Phe Tyr Lys Asp Ser Lys Ser Trp Glu Asp
145 150 155 160

Cys Lys Tyr Phe Cys Leu Ser Glu Asn Ser Thr Met Leu Lys Ile Asn
165 170 175

Lys Gln Glu Asp Leu Glu Phe Ala Ala Ser Gln Ser Tyr Ser Glu Phe
180 185 190

Phe Tyr Ser Tyr Trp Thr Gly Leu Leu Arg Pro Asp Ser Gly Lys Ala
195 200 205

Trp Leu Trp Met Asp Gly Thr Pro Phe Thr Ser Glu Leu Phe His Ile
210 215 220

Ile Ile Asp Val Thr Ser Pro Arg Ser Arg Asp Cys Val Ala Ile Leu
225 230 235 240

Asn Gly Met Ile Phe Ser Lys Asp Cys Lys Glu Leu Lys Arg Cys Val
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Cys Glu Arg Arg Ala Gly Met Val Lys Pro Glu Ser Leu His Val Pro
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Pro Glu Thr Leu Gly Glu Gly Asp
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Ser Thr Met Asp Met Leu Asp Asp Asp Gly Asp Thr Thr Met Ser Leu
10 15 20

cat tct caa gcc tct gcc aca act cgg cat cca gag ccc cgg cgc aca 151
His Ser Gln Ala Ser Ala Thr Thr Arg His Pro Glu Pro Arg Arg Thr
25 30 35

gag cac agg gct ccc tct tca acg tgg cga cca gtg gcc ctg acc ctg 199
Glu His Arg Ala Pro Ser Ser Thr Trp Arg Pro Val Ala Leu Thr Leu
40 45 50

ctg act ttg tgc ttg gtg ctg ctg ata ggg ctg gca gcc ctg ggg ctt 247
Leu Thr Leu Cys Leu Val Leu Leu Ile Gly Leu Ala Ala Leu Gly Leu
55 60 65 70

ttg ttt ttt cag tac tac cag ctc tcc aat act ggt caa gac acc att 295

Leu	Phe	Phe	Gln	Tyr	Tyr	Gln	Leu	Ser	Asn	Thr	Gly	Gln	Asp	Thr	Ile	
				75					80					85		
tct	caa	atg	gaa	gaa	aga	tta	gga	aat	acg	tcc	caa	gag	ttg	caa	tct	343
Ser	Gln	Met	Glu	Glu	Arg	Leu	Gly	Asn	Thr	Ser	Gln	Glu	Leu	Gln	Ser	
			90					95					100			
ctt	caa	gtc	cag	aat	ata	aag	ctt	gca	gga	agt	ctg	cag	cat	gtg	gct	391
Leu	Gln	Val	Gln	Asn	Ile	Lys	Leu	Ala	Gly	Ser	Leu	Gln	His	Val	Ala	
		105					110					115				
gaa	aaa	ctc	tgt	cgt	gag	ctg	tat	aac	aaa	gct	gga	ggc	tat	aca	aga	439
Glu	Lys	Leu	Cys	Arg	Glu	Leu	Tyr	Asn	Lys	Ala	Gly	Gly	Tyr	Thr	Arg	
	120					125					130					
aac	atg	gtg	cca	gca	tct	gct	tct	tct	gag	agc	ctc	agg	cag	ctt	cca	487
Asn	Met	Val	Pro	Ala	Ser	Ala	Ser	Ser	Glu	Ser	Leu	Arg	Gln	Leu	Pro	
135					140					145					150	
cac	atg	ggg	gaa	agt	gca	gca	gca	cac	agg	tgc	agc	cct	tgt	aca	gaa	535
His	Met	Gly	Glu	Ser	Ala	Ala	Ala	His	Arg	Cys	Ser	Pro	Cys	Thr	Glu	
				155					160					165		
caa	tgg	aaa	tgg	cat	gga	gac	aat	tgc	tac	cag	ttc	tat	aaa	gac	agc	583
Gln	Trp	Lys	Trp	His	Gly	Asp	Asn	Cys	Tyr	Gln	Phe	Tyr	Lys	Asp	Ser	
			170				175						180			
aaa	agt	tgg	gag	gac	tgt	aaa	tat	ttc	tgc	ctt	agt	gaa	aac	tct	acc	631
Lys	Ser	Trp	Glu	Asp	Cys	Lys	Tyr	Phe	Cys	Leu	Ser	Glu	Asn	Ser	Thr	
		185					190					195				
atg	ctg	aag	ata	aac	aaa	caa	gaa	gac	ctg	gaa	ttt	gcc	gcg	tct	cag	679
Met	Leu	Lys	Ile	Asn	Lys	Gln	Glu	Asp	Leu	Glu	Phe	Ala	Ala	Ser	Gln	
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agc	tac	tct	gag	ttt	ttc	tac	tct	tat	tgg	aca	ggg	ctt	ttg	ggc	cct	727
Ser	Tyr	Ser	Glu	Phe	Phe	Tyr	Ser	Tyr	Trp	Thr	Gly	Leu	Leu	Arg	Pro	
215					220					225					230	
gac	agt	ggc	aag	gcc	tgg	ctg	tgg	atg	gat	gga	acc	cct	ttc	act	tct	775
Asp	Ser	Gly	Lys	Ala	Trp	Leu	Trp	Met	Asp	Gly	Thr	Pro	Phe	Thr	Ser	
				235					240					245		
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Glu	Leu	Phe	His	Ile	Ile	Ile	Asp	Val	Thr	Ser	Pro	Arg	Ser	Arg	Asp	
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Cys	Val	Ala	Ile	Leu	Asn	Gly	Met	Ile	Phe	Ser	Lys	Asp	Cys	Lys	Glu	
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Pro Val Ala Leu Thr Leu Leu Thr Leu Cys Leu Val Leu Leu Ile Gly
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Leu Ala Ala Leu Gly Leu Leu Phe Phe Gln Tyr Tyr Gln Leu Ser Asn
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Thr Gly Gln Asp Thr Ile Ser Gln Met Glu Glu Arg Leu Gly Asn Thr
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Met Gln Ala Lys Tyr Ser Ser Thr Arg Asp
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Met Leu Asp Asp Asp Gly Asp Thr Thr Met Ser Leu His Ser Gln Ala
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Ser Ala Thr Thr Arg His Pro Glu Pro Arg Arg Thr Val Phe Gln Tyr
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Tyr Gln Leu Ser Asn Thr Gly Gln Asp Thr Ile Ser Gln Met Glu Glu
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Arg Leu Gly Asn Thr Ser Gln Glu Leu Gln Ser Leu Gln Val Gln Asn
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Glu Leu Tyr Asn Lys Ala Gly Ala His Arg Cys Ser Pro Cys Thr Glu	
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Gln Trp Lys Trp His Gly Asp Asn Cys Tyr Gln Phe Tyr Lys Asp Ser	
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aaa agt tgg gag gac tgt aaa tat ttc tgc ctt agt gaa aac tct acc	495
Lys Ser Trp Glu Asp Cys Lys Tyr Phe Cys Leu Ser Glu Asn Ser Thr	
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Met Leu Lys Ile Asn Lys Gln Glu Asp Leu Glu Phe Ala Ala Ser Gln	
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Ser Tyr Ser Glu Phe Phe Tyr Ser Tyr Trp Thr Gly Leu Leu Arg Pro	
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Glu Leu Phe His Ile Ile Ile Asp Val Thr Ser Pro Arg Ser Arg Asp	
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Cys Val Ala Ile Leu Asn Gly Met Ile Phe Ser Lys Asp Cys Lys Glu	
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Ser Leu His Val Pro Pro Glu Thr Leu Gly Glu Gly Asp	
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 Gly Gln Asp Thr Ile Ser Gln Met Glu Glu Arg Leu Gly Asn Thr Ser
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 Gln Glu Leu Gln Ser Leu Gln Val Gln Asn Ile Lys Leu Ala Gly Ser
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 Gly Ala His Arg Cys Ser Pro Cys Thr Glu Gln Trp Lys Trp His Gly
 100 105 110

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Asp Asn Cys Tyr Gln Phe Tyr Lys Asp Ser Lys Ser Trp Glu Asp Cys
115 120 125

Lys Tyr Phe Cys Leu Ser Glu Asn Ser Thr Met Leu Lys Ile Asn Lys
130 135 140

Gln Glu Asp Leu Glu Phe Ala Ala Ser Gln Ser Tyr Ser Glu Phe Phe
145 150 155 160

Tyr Ser Tyr Trp Thr Gly Leu Leu Arg Pro Asp Ser Gly Lys Ala Trp
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Leu Trp Met Asp Gly Thr Pro Phe Thr Ser Glu Leu Phe His Ile Ile
180 185 190

Ile Asp Val Thr Ser Pro Arg Ser Arg Asp Cys Val Ala Ile Leu Asn
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gccaaggcct tccctgcc atg cga cct gtc agt gtc tgg cag tgg agc ccc 231
Met Arg Pro Val Ser Val Trp Gln Trp Ser Pro
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Trp Gly Leu Leu Leu Cys Leu Leu Cys Ser Ser Cys Leu Gly Ser Pro
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Ser Pro Ser Thr Gly Pro Glu Lys Lys Ala Gly Ser Gln Gly Leu Arg
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Phe Arg Leu Ala Gly Phe Pro Arg Lys Pro Tyr Glu Gly Arg Val Glu	
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Ile Gln Arg Ala Gly Glu Trp Gly Thr Ile Cys Asp Asp Asp Phe Thr	
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Leu Gln Ala Ala His Ile Leu Cys Arg Glu Leu Gly Phe Thr Glu Ala	
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Thr Gly Trp Thr His Ser Ala Lys Tyr Gly Pro Gly Thr Gly Arg Ile	
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Cys Ala Ser Arg Gly Trp Gly Asn Ser Asp Cys Thr His Asp Glu Asp	
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Ala Gly Val Ile Cys Lys Asp Gln Arg Leu Pro Gly Phe Ser Asp Ser	
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Asn Val Ile Glu Val Glu His His Leu Gln Val Glu Glu Val Arg Ile	
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Arg Pro Ala Val Gly Trp Gly Arg Arg Pro Leu Pro Val Thr Glu Gly	
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Leu Val Glu Val Arg Leu Pro Asp Gly Trp Ser Gln Val Cys Asp Lys	
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Gly Trp Ser Ala His Asn Ser His Val Val Cys Gly Met Leu Gly Phe	
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Pro Ser Glu Lys Arg Val Asn Ala Ala Phe Tyr Arg Leu Leu Ala Gln	
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Arg Gln Gln His Ser Phe Gly Leu His Gly Val Ala Cys Val Gly Thr	
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His Glu Cys His Gly His Tyr His Ser Met Asp Phe Phe Thr His Tyr	
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Phe Pro Arg Lys Pro Tyr Glu Gly Arg Val Glu Ile Gln Arg Ala Gly
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Glu Trp Gly Thr Ile Cys Asp Asp Asp Phe Thr Leu Gln Ala Ala His
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Ser Ala Lys Tyr Gly Pro Gly Thr Gly Arg Ile Trp Leu Asp Asn Leu
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Trp Gly Asn Ser Asp Cys Thr His Asp Glu Asp Ala Gly Val Ile Cys
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Lys Asp Gln Arg Leu Pro Gly Phe Ser Asp Ser Asn Val Ile Glu Val
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Glu His His Leu Gln Val Glu Glu Val Arg Ile Arg Pro Ala Val Gly
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Trp Gly Arg Arg Pro Leu Pro Val Thr Glu Gly Leu Val Glu Val Arg

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Asn Ser His Val Val Cys Gly Met Leu Gly Phe Pro Ser Glu Lys Arg		
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Val Asn Ala Ala Phe Tyr Arg Leu Leu Ala Gln Arg Gln Gln His Ser		
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Phe Gly Leu His Gly Val Ala Cys Val Gly Thr Glu Ala His Leu Ser		
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Leu Cys Ser Leu Glu Phe Tyr Arg Ala Asn Asp Thr Ala Arg Cys Pro		
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Gly Gly Gly Pro Ala Val Val Ser Cys Val Pro Gly Pro Val Tyr Ala		
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Ala Ser Ser Gly Gln Lys Lys Gln Gln Gln Ser Lys Pro Gln Gly Glu		
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Val Arg Val Arg Leu Lys Gly Gly Ala His Pro Gly Glu Gly Arg Val		
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Glu Val Leu Lys Ala Ser Thr Trp Gly Thr Val Cys Tyr Arg Lys Trp		
	325	330
Asp Leu His Ala Ala Ser Val Val Cys Arg Glu Leu Gly Phe Gly Ser		
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Ala Arg Glu Ala Leu Ser Gly Ala Arg Met Gly Gln Gly Met Gly Ala		
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Ile His Leu Ser Glu Val Arg Cys Ser Gly Gln Glu Leu Ser Leu Trp		
	370	375
Lys Cys Pro His Lys Asn Ile Thr Ala Glu Asp Cys Ser His Ser Gln		
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Asp Ala Gly Val Arg Cys Asn Leu Pro Tyr Thr Gly Ala Glu Thr Arg		
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Ile Arg Leu Ser Gly Gly Arg Ser Gln His Glu Gly Arg Val Glu Val		
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Asn Ile Thr Glu Val Val Met Ser Gly Val Arg Cys Thr Gly Thr Glu
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Leu Ser Leu Asp Gln Cys Ala His His Gly Thr His Ile Thr Cys Lys
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His Tyr His Ser Met Asp Phe Phe Thr His Tyr Asp Ile Leu Thr Pro
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Asp Ile Asp Cys Gln Trp Ile Asp Ile Thr Asp Val Lys Pro Gly Asn
675 680 685

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cctgcc atg cga cct gtc agt gtc tgg cag tgg agc ccc tgg ggg ctg 168
Met Arg Pro Val Ser Val Trp Gln Trp Ser Pro Trp Gly Leu
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Leu Leu Cys Leu Leu Cys Ser Ser Cys Leu Gly Ser Pro Ser Pro Ser
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Thr Gly Pro Glu Lys Lys Ala Gly Ser Gln Gly Leu Arg Phe Arg Leu
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Ala Gly Phe Pro Arg Lys Pro Tyr Glu Gly Arg Val Glu Ile Gln Arg
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Ala Gly Glu Trp Gly Thr Ile Cys Asp Asp Asp Phe Thr Leu Gln Ala
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gcc cac atc ctc tgc cgg gag ctg ggc ttc aca gag gcc aca ggc tgg 408
Ala His Ile Leu Cys Arg Glu Leu Gly Phe Thr Glu Ala Thr Gly Trp
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Ile	Cys	Lys	Asp	Gln	Arg	Leu	Pro	Gly	Phe	Ser	Asp	Ser	Asn	Val	Ile	
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att agc agc aaa tgg cac tgc gac tct gat gac gac tgt ggg gac Ile Ser Ser Lys Trp His Cys Asp Ser Asp Asp Asp Cys Gly Asp 1020 1025 1030	3957
ggg agt gat gag gtg ggc tgt gtt cac tct tgc ttt gat aat cag Gly Ser Asp Glu Val Gly Cys Val His Ser Cys Phe Asp Asn Gln 1035 1040 1045	4002
ttc aga tgt tcc agt ggc aga tgc atc cca ggc cac tgg gcc tgt Phe Arg Cys Ser Ser Gly Arg Cys Ile Pro Gly His Trp Ala Cys 1050 1055 1060	4047
gat ggt gac aat gac tgt ggg gac ttc agt gat gaa gcc cag atc Asp Gly Asp Asn Asp Cys Gly Asp Phe Ser Asp Glu Ala Gln Ile 1065 1070 1075	4092
aat tgt act aaa gaa gag att cat tct cct gct ggt tgt aac gga Asn Cys Thr Lys Glu Glu Ile His Ser Pro Ala Gly Cys Asn Gly 1080 1085 1090	4137
aat gaa ttt cag tgc cac cct gat ggt aat tgc gtt cct gat ttg Asn Glu Phe Gln Cys His Pro Asp Gly Asn Cys Val Pro Asp Leu 1095 1100 1105	4182
tgg cgc tgt gat gga gaa aaa gac tgt gaa gat ggt agt gat gaa Trp Arg Cys Asp Gly Glu Lys Asp Cys Glu Asp Gly Ser Asp Glu 1110 1115 1120	4227
aaa ggt tgc aat ggt acc ata cga ttg tgt gac cac aaa acc aag Lys Gly Cys Asn Gly Thr Ile Arg Leu Cys Asp His Lys Thr Lys 1125 1130 1135	4272

3579 3627 3675 3723 3771 3819 3867 3912 3957 4002 4047 4092 4137 4182 4227 4272

ttt	tcc	tgt	tgg	agt	aca	ggg	aga	tgc	atc	aac	aaa	gca	tgg	gtg	4317
Phe	Ser	Cys	Trp	Ser	Thr	Gly	Arg	Cys	Ile	Asn	Lys	Ala	Trp	Val	
		1140					1145					1150			
tgt	gat	gga	gat	att	gat	tgc	gaa	gat	cag	tca	gat	gaa	gat	gac	4362
Cys	Asp	Gly	Asp	Ile	Asp	Cys	Glu	Asp	Gln	Ser	Asp	Glu	Asp	Asp	
		1155					1160					1165			
tgt	gac	agt	ttc	ttg	tgt	gga	cca	ccc	aag	cat	cct	tgt	gct	aat	4407
Cys	Asp	Ser	Phe	Leu	Cys	Gly	Pro	Pro	Lys	His	Pro	Cys	Ala	Asn	
		1170					1175					1180			
gac	acc	tca	gtc	tgc	ctg	cag	cca	gag	aaa	ctc	tgc	aat	ggg	aaa	4452
Asp	Thr	Ser	Val	Cys	Leu	Gln	Pro	Glu	Lys	Leu	Cys	Asn	Gly	Lys	
		1185					1190					1195			
aag	gat	tgt	cct	gat	ggc	tct	gat	gaa	ggc	tat	ctc	tgt	gat	gag	4497
Lys	Asp	Cys	Pro	Asp	Gly	Ser	Asp	Glu	Gly	Tyr	Leu	Cys	Asp	Glu	
		1200					1205					1210			
tgt	tcg	ctg	aac	aat	gga	ggc	tgt	agc	aac	cac	tgt	tct	gtt	gtt	4542
Cys	Ser	Leu	Asn	Asn	Gly	Gly	Cys	Ser	Asn	His	Cys	Ser	Val	Val	
		1215					1220					1225			
cct	gga	aga	gga	att	gtc	tgt	tcc	tgc	cct	gaa	gga	ctt	caa	ctc	4587
Pro	Gly	Arg	Gly	Ile	Val	Cys	Ser	Cys	Pro	Glu	Gly	Leu	Gln	Leu	
		1230					1235					1240			
aac	aaa	gac	aat	aaa	aca	tgt	gaa	att	gtg	gat	tat	tgt	agc	aat	4632
Asn	Lys	Asp	Asn	Lys	Thr	Cys	Glu	Ile	Val	Asp	Tyr	Cys	Ser	Asn	
		1245					1250					1255			
cat	cta	aag	tgc	agc	caa	gta	tgt	gag	cag	cac	aag	cac	aca	gtc	4677
His	Leu	Lys	Cys	Ser	Gln	Val	Cys	Glu	Gln	His	Lys	His	Thr	Val	
		1260					1265					1270			
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Lys	Cys	Ser	Cys	Tyr	Glu	Gly	Trp	Lys	Leu	Asp	Val	Asp	Gly	Glu	
		1275					1280					1285			
agt	tgt	aca	agt	gtt	gat	cct	ttt	gaa	gca	ttc	atc	atc	ttt	tct	4767
Ser	Cys	Thr	Ser	Val	Asp	Pro	Phe	Glu	Ala	Phe	Ile	Ile	Phe	Ser	
		1290					1295					1300			
att	cgt	cat	gag	atc	aga	agg	att	gat	ctt	cac	aaa	aga	gac	tat	4812
Ile	Arg	His	Glu	Ile	Arg	Arg	Ile	Asp	Leu	His	Lys	Arg	Asp	Tyr	
		1305					1310					1315			
agt	cta	ctt	gtt	cct	gga	ttg	aga	aac	aca	ata	gca	ctt	gat	ttt	4857
Ser	Leu	Leu	Val	Pro	Gly	Leu	Arg	Asn	Thr	Ile	Ala	Leu	Asp	Phe	
		1320					1325					1330			
cac	ttc	aat	caa	agt	tta	ctt	tat	tgg	aca	gat	gtt	gta	gaa	gac	4902

aca gtc gac	tgg ata gca gga aac	ata tac tgg ata gac	agc aat	5037
Thr Val Asp	Trp Ile Ala Gly Asn	Ile Tyr Trp Ile Asp	Ser Asn	
1380	1385	1390		
ctg gac caa	atc gaa gtg gcc aaa	cta gat ggc tcc cta	aga act	5082
Leu Asp Gln	Ile Glu Val Ala Lys	Leu Asp Gly Ser Leu	Arg Thr	
1395	1400	1405		
aca cta ata	gca gga gcc atg gaa	cac ccc agg gcc att	gct ttg	5127
Thr Leu Ile	Ala Gly Ala Met Glu	His Pro Arg Ala Ile	Ala Leu	
1410	1415	1420		
gac cca aga	tat gga att ctt ttc	tgg aca gac tgg gat	gca aat	5172
Asp Pro Arg	Tyr Gly Ile Leu Phe	Trp Thr Asp Trp Asp	Ala Asn	
1425	1430	1435		
ttt cct cgc	att gaa tct gcc tct	atg agt ggt gct ggg	aga aaa	5217
Phe Pro Arg	Ile Glu Ser Ala Ser	Met Ser Gly Ala Gly	Arg Lys	
1440	1445	1450		
acc atc tat	aaa gac atg aaa act	ggg gct tgg cct aat	gga cta	5262
Thr Ile Tyr	Lys Asp Met Lys Thr	Gly Ala Trp Pro Asn	Gly Leu	
1455	1460	1465		
act gtg gac	cac ttt gag aaa agg	ata gtg tgg aca gac	gcc agg	5307
Thr Val Asp	His Phe Glu Lys Arg	Ile Val Trp Thr Asp	Ala Arg	
1470	1475	1480		
tca gat gct	att tat tca gcc ctc	tat gat gga aca aac	atg ata	5352
Ser Asp Ala	Ile Tyr Ser Ala Leu	Tyr Asp Gly Thr Asn	Met Ile	
1485	1490	1495		
gaa atc atc	cga ggt cat gaa tac	ctt tcc cat ccc ttt	gct gtg	5397
Glu Ile Ile	Arg Gly His Glu Tyr	Leu Ser His Pro Phe	Ala Val	
1500	1505	1510		
tct cta tat	ggg agt gaa gtc tac	tgg aca gac tgg agg	acc aac	5442
Ser Leu Tyr	Gly Ser Glu Val Tyr	Trp Thr Asp Trp Arg	Thr Asn	
1515	1520	1525		
aca ttg tcc	aaa gcc aat aag tgg	aca ggg cag aat gtc	agt gtg	5487
Thr Leu Ser	Lys Ala Asn Lys Trp	Thr Gly Gln Asn Val	Ser Val	
1530	1535	1540		
att cag aaa	acc agt gca cag cca	ttt gac ctt cag ata	tac cat	5532
Ile Gln Lys	Thr Ser Ala Gln Pro	Phe Asp Leu Gln Ile	Tyr His	
1545	1550	1555		
ccc agt cgc	cag cca cag gct ccc	aat cct tgt gca gct	aat gat	5577
Pro Ser Arg	Gln Pro Gln Ala Pro	Asn Pro Cys Ala Ala	Asn Asp	
1560	1565	1570		
ggc aaa ggc	ccc tgc tct cac atg	tgt cta atc aat cac	aat agg	5622
Gly Lys Gly	Pro Cys Ser His Met	Cys Leu Ile Asn His	Asn Arg	
1575	1580	1585		
agt gct gcc	tgt gcg tgc ccc cac	ttg atg aag ctt tct	tca gac	5667
Ser Ala Ala	Cys Ala Cys Pro His	Leu Met Lys Leu Ser	Ser Asp	
1590	1595	1600		
aag aag acc	tgc tat gaa atg aaa	aaa ttt ctt ctt tat	gca aga	5712
Lys Lys Thr	Cys Tyr Glu Met Lys	Lys Phe Leu Leu Tyr	Ala Arg	
1605	1610	1615		

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7152

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Thr	Asp	Lys	Ile	Glu	Arg	Ile	Asp	Leu	Glu	Thr	Gly	Gly	Asn	Arg	
		2100					2105					2110			
gag	atg	gtg	ctg	tca	gga	agc	aat	gtg	gat	atg	ttt	tca	gtt	gca	7242
Glu	Met	Val	Leu	Ser	Gly	Ser	Asn	Val	Asp	Met	Phe	Ser	Val	Ala	
		2115					2120					2125			
gtc	ttt	ggg	gct	tac	atc	tac	tgg	tct	gac	aga	gca	cat	gca	aac	7287
Val	Phe	Gly	Ala	Tyr	Ile	Tyr	Trp	Ser	Asp	Arg	Ala	His	Ala	Asn	
		2130					2135					2140			
ggg	tct	gtc	aga	agg	ggc	cac	aag	aat	gat	gcc	aca	gaa	acg	ata	7332
Gly	Ser	Val	Arg	Arg	Gly	His	Lys	Asn	Asp	Ala	Thr	Glu	Thr	Ile	
		2145					2150					2155			
acc	atg	aga	acc	ggc	ctt	gga	gtc	aac	ctg	aag	gag	gtt	aaa	ata	7377
Thr	Met	Arg	Thr	Gly	Leu	Gly	Val	Asn	Leu	Lys	Glu	Val	Lys	Ile	
		2160					2165					2170			
ttt	aac	cga	gta	aga	gag	aaa	ggg	acc	aat	gtt	tgt	gcc	agg	gac	7422
Phe	Asn	Arg	Val	Arg	Glu	Lys	Gly	Thr	Asn	Val	Cys	Ala	Arg	Asp	
		2175					2180					2185			
aat	ggc	ggc	tgt	aag	caa	ctc	tgt	ctt	tat	cga	gga	aat	tcc	cgg	7467
Asn	Gly	Gly	Cys	Lys	Gln	Leu	Cys	Leu	Tyr	Arg	Gly	Asn	Ser	Arg	
		2190					2195					2200			
aga	act	tgt	gct	tgt	gcc	cat	gga	tat	ttg	gca	gaa	gat	gga	gtt	7512
Arg	Thr	Cys	Ala	Cys	Ala	His	Gly	Tyr	Leu	Ala	Glu	Asp	Gly	Val	
		2205					2210					2215			
act	tgc	ctg	agg	cat	gaa	ggc	tat	tta	ctg	tat	tca	gga	aga	aca	7557
Thr	Cys	Leu	Arg	His	Glu	Gly	Tyr	Leu	Leu	Tyr	Ser	Gly	Arg	Thr	
		2220					2225					2230			
ata	tta	aaa	agt	ata	cat	ctt	tct	gat	gaa	acc	aat	tta	aat	tcc	7602
Ile	Leu	Lys	Ser	Ile	His	Leu	Ser	Asp	Glu	Thr	Asn	Leu	Asn	Ser	
		2235					2240					2245			
cca	ata	agg	cca	tat	gag	aat	cca	cgt	tat	ttc	aag	aat	gtc	ata	7647
Pro	Ile	Arg	Pro	Tyr	Glu	Asn	Pro	Arg	Tyr	Phe	Lys	Asn	Val	Ile	
		2250					2255					2260			
gcc	ttg	gct	ttt	gac	tat	aat	caa	aga	aga	aaa	ggc	acc	aac	cga	7692
Ala	Leu	Ala	Phe	Asp	Tyr	Asn	Gln	Arg	Arg	Lys	Gly	Thr	Asn	Arg	
		2265					2270					2275			
atc	ttt	tac	agt	gat	gca	cac	ttt	gga	aat	ata	cag	ctt	att	aaa	7737
Ile	Phe	Tyr	Ser	Asp	Ala	His	Phe	Gly	Asn	Ile	Gln	Leu	Ile	Lys	
		2280					2285					2290			
gac	aac	tgg	gaa	gac	aga	caa	gta	att	gtt	gaa	aat	gtg	ggc	tct	778

act Thr	cgg Arg	cct Pro 2340	gga Gly	gca Ala	ttt Phe	gac Asp	agg Arg 2345	gaa Glu	gct Ala	gtc Val	atc Ile	acc Thr 2350	atg Met	tca Ser	7917
gaa Glu	gat Asp	gac Asp 2355	cat His	cca Pro	cat His	gtg Val	cta Leu 2360	gcc Ala	ttg Leu	gat Asp	gaa Glu	tgt Cys 2365	caa Gln	aat Asn	7962
tta Leu	atg Met	ttt Phe 2370	tgg Trp	acc Thr	aac Asn	tgg Trp	aat Asn 2375	gaa Glu	caa Gln	cat His	cca Pro	agt Ser 2380	atc Ile	atg Met	8007
aga Arg	tct Ser	act Thr 2385	ctg Leu	act Thr	ggg Gly	aaa Lys	aat Asn 2390	gct Ala	caa Gln	gtg Val	gtg Val	gtc Val 2395	agt Ser	aca Thr	8052
gac Asp	ata Ile	ctc Leu 2400	act Thr	cca Pro	aat Asn	gga Gly	ctt Leu 2405	act Thr	atc Ile	gac Asp	tac Tyr	cgt Arg 2410	gca Ala	gag Glu	8097
aag Lys	ctg Leu	tat Tyr 2415	ttc Phe	tca Ser	gat Asp	ggc Gly	agt Ser 2420	cta Leu	gga Gly	aaa Lys	att Ile	gaa Glu 2425	agg Arg	tgt Cys	8142
gaa Glu	tac Tyr	gat Asp 2430	gga Gly	tcc Ser	cag Gln	aga Arg	cat His 2435	gtg Val	ata Ile	gtt Val	aaa Lys	tct Ser 2440	ggg Gly	cca Pro	8187
ggg Gly	act Thr	ttc Phe 2445	ctc Leu	agt Ser	ttg Leu	gct Ala	gtt Val 2450	tat Tyr	gac Asp	aat Asn	tat Tyr	ata Ile 2455	ttc Phe	tgg Trp	8232
tcg Ser	gac Asp	tgg Trp 2460	gga Gly	aga Arg	aga Arg	gct Ala	ata Ile 2465	ctg Leu	cgg Arg	tcc Ser	aac Asn	aag Lys 2470	tac Tyr	aca Thr	8277
gga Gly	gga Gly	gat Asp 2475	aca Thr	aaa Lys	att Ile	ctt Leu	cgt Arg 2480	tcc Ser	gat Asp	att Ile	cca Pro	cat His 2485	cag Gln	cca Pro	8322
atg Met	gga Gly	atc Ile 2490	ata Ile	gct Ala	gtt Val	gcc Ala	aat Asn 2495	gac Asp	acc Thr	aat Asn	agc Ser	tgt Cys 2500	gaa Glu	ctt Leu	8367
tct Ser	cca Pro	tgt Cys 2505	gca Ala	tta Leu	ttg Leu	aat Asn	gga Gly 2510	ggc Gly	tgc Cys	cat His	gac Asp	ttg Leu 2515	tgc Cys	ctt Leu	8412
tta Leu	act Thr	ccc Pro 2520	aat Asn	ggg Gly	aga Arg	gtg Val	aat Asn 2525	tgt Cys	tcc Ser	tgc Cys	aga Arg	ggg Gly 2530	gac Asp	cga Arg	8457
ata Ile	ttg Leu	cta Leu 2535	gag Glu	gac Asp	aac Asn	aga Arg	tgt Cys 2540	gtg Val	act Thr	aaa Lys	aat Asn	tcc Ser 2545	tcc Ser	tgc Cys	8502
aac Asn	gct Ala	tat Tyr 2550	tcg Ser	gag Glu	ttt Phe	gaa Glu	tgt Cys 2555	gga Gly	aat Asn	ggt Gly	gag Glu	tgc Cys 2560	att Ile	gac Asp	8547
tac Tyr	cag Gln	ctc Leu 2565	acc Thr	tgt Cys	gat Asp	ggc Gly	att Ile 2570	cct Pro	cac His	tgt Cys	aaa Lys	gat Asp 2575	aaa Lys	tca Ser	8592

gat gaa aaa ctg ctc tac tgt gaa aac aga agc tgt cga aga ggc	8637
Asp Glu Lys Leu Leu Tyr Cys Glu Asn Arg Ser Cys Arg Arg Gly	
2580 2585 2590	
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Phe Lys Pro Cys Tyr Asn Arg Arg Cys Ile Pro His Gly Lys Leu	
2595 2600 2605	
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Cys Asp Gly Glu Asn Asp Cys Gly Asp Asn Ser Asp Glu Leu Asp	
2610 2615 2620	
tgt aaa gtt tca acc tgt gcc acg gtt gag ttc cgc tgt gca gat	8772
Cys Lys Val Ser Thr Cys Ala Thr Val Glu Phe Arg Cys Ala Asp	
2625 2630 2635	
ggg act tgt att cca aga tca gca cga tgc aac cag aac ata gat	8817
Gly Thr Cys Ile Pro Arg Ser Ala Arg Cys Asn Gln Asn Ile Asp	
2640 2645 2650	
tgt gca gat gct tca gat gaa aag aac tgc aat aac aca gac tgc	8862
Cys Ala Asp Ala Ser Asp Glu Lys Asn Cys Asn Asn Thr Asp Cys	
2655 2660 2665	
aca cat ttc tat aag ctt gga gtg aaa acc aca ggg ttc ata aga	8907
Thr His Phe Tyr Lys Leu Gly Val Lys Thr Thr Gly Phe Ile Arg	
2670 2675 2680	
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Cys Asn Ser Thr Ser Leu Cys Val Leu Pro Thr Trp Ile Cys Asp	
2685 2690 2695	
ggg tct aat gac tgt gga gac tat tca gat gaa tta aag tgc cca	8997
Gly Ser Asn Asp Cys Gly Asp Tyr Ser Asp Glu Leu Lys Cys Pro	
2700 2705 2710	
gtt cag aac aaa cac aaa tgt gaa gaa aat tat ttt agt tgt cct	9042
Val Gln Asn Lys His Lys Cys Glu Glu Asn Tyr Phe Ser Cys Pro	
2715 2720 2725	
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Ser Gly Arg Cys Ile Leu Asn Thr Trp Ile Cys Asp Gly Gln Lys	
2730 2735 2740	
gat tgt gag gat gga cgt gat gaa ttc cac tgt gat tct tct tgc	9132
Asp Cys Glu Asp Gly Arg Asp Glu Phe His Cys Asp Ser Ser Cys	
2745 2750 2755	
tct tgg aac caa ttt gct tgt tcc gca caa aaa tgt att tct aag	9177
Ser Trp Asn Gln Phe Ala Cys Ser Ala Gln Lys Cys Ile Ser Lys	
2760 2765 2770	
cat tgg att tgt gat gga gaa gat gac tgt ggg gat ggg tta gat	9222
His Trp Ile Cys Asp Gly Glu Asp Asp Cys Gly Asp Gly Leu Asp	
2775 2780 2785	
gaa agt gac agc att tgt ggt gcc ata acc tgt gct gct gac atg	9267
Glu Ser Asp Ser Ile Cys Gly Ala Ile Thr Cys Ala Ala Asp Met	
2790 2795 2800	
ttc agc tgc cag ggc tct cgt gcc tgc gtg ccc cga cat tgg ctt	9312
Phe Ser Cys Gln Gly Ser Arg Ala Cys Val Pro Arg His Trp Leu	
2805 2810 2815	

PEPTIDE SEQUENCE

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aca gca ggc tgc gct ccc aat aat aca tgt gat gaa aat gct ttc Thr Ala Gly Cys Ala Pro Asn Asn Thr Cys Asp Glu Asn Ala Phe 2835 2840 2845	9402
atg tgc cat aat aaa gta tgc att ccc aag caa ttt gtt tgt gac Met Cys His Asn Lys Val Cys Ile Pro Lys Gln Phe Val Cys Asp 2850 2855 2860	9447
cat gat gac gac tgt gga gat ggc tct gat gag tca ccg cag tgt His Asp Asp Asp Cys Gly Asp Gly Ser Asp Glu Ser Pro Gln Cys 2865 2870 2875	9492
gga tac cga cag tgt ggt aca gaa gaa ttt agt tgt gct gat ggg Gly Tyr Arg Gln Cys Gly Thr Glu Glu Phe Ser Cys Ala Asp Gly 2880 2885 2890	9537
cgg tgt ctt cta aat act caa tgg cag tgt gat gga gac ttt gac Arg Cys Leu Leu Asn Thr Gln Trp Gln Cys Asp Gly Asp Phe Asp 2895 2900 2905	9582
tgt cct gac cat tct gat gaa gca cct tta aac cca aag tgt aaa Cys Pro Asp His Ser Asp Glu Ala Pro Leu Asn Pro Lys Cys Lys 2910 2915 2920	9627
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ggc agg tgc att ccc agt gga ggt ctt tgt gac aat aag gat gac Gly Arg Cys Ile Pro Ser Gly Gly Leu Cys Asp Asn Lys Asp Asp 2940 2945 2950	9717
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ccg gtc agt tat aag tgc aaa tgc tgg cct gga ttc caa ctg aag Pro Val Ser Tyr Lys Cys Lys Cys Trp Pro Gly Phe Gln Leu Lys 2985 2990 2995	9852
gat gac ggc aaa aca tgt gta gac att gat gaa tgc tct tca ggc Asp Asp Gly Lys Thr Cys Val Asp Ile Asp Glu Cys Ser Ser Gly 3000 3005 3010	9897
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tgc ctc tgt aca gat ggg tat gaa ata caa cct gat aac cca aat Cys Leu Cys Thr Asp Gly Tyr Glu Ile Gln Pro Asp Asn Pro Asn 3030 3035 3040	9987
ggc tgc aaa tcg ctc tca gat gaa gaa cct ttt tta att ctt gct Gly Cys Lys Ser Leu Ser Asp Glu Glu Pro Phe Leu Ile Leu Ala 3045 3050 3055	10032

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Asp His His Glu Ile Arg Lys Ile Ser Thr Asp Gly Ser Asn Tyr	
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Thr Leu Leu Lys Gln Gly Leu Asn Asn Val Ile Ala Ile Asp Phe	
3075 3080 3085	
gat tac aga gaa gaa ttc atc tat tgg atc gat tct agc cga ccc	10167
Asp Tyr Arg Glu Glu Phe Ile Tyr Trp Ile Asp Ser Ser Arg Pro	
3090 3095 3100	
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Asn Gly Ser Arg Ile Asn Arg Met Cys Leu Asn Gly Ser Asp Ile	
3105 3110 3115	
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Lys Val Val His Asn Thr Ala Val Pro Asn Ala Leu Ala Val Asp	
3120 3125 3130	
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Trp Ile Gly Lys Asn Leu Tyr Trp Ser Asp Thr Glu Lys Arg Ile	
3135 3140 3145	
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Ile Glu Val Ser Lys Leu Asn Gly Leu Tyr Pro Thr Ile Leu Val	
3150 3155 3160	
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Ser Lys Arg Leu Lys Phe Pro Arg Asp Leu Ser Leu Asp Pro Gln	
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Gln Phe Arg Cys Lys Asn Lys Ala His Cys Ile Pro Ile Arg Trp	
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Leu Cys Asp Gly Ile His Asp Cys Val Asp Gly Ser Asp Glu Glu	
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Thr Tyr Lys	Ala Arg Pro Cys	Lys Lys Asp Glu Phe Ala	Cys Ser	
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Asn Lys Lys	Cys Ile Pro Met	Asp Leu Gln Cys Asp	Leu Asp	
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Asp Cys Gly	Asp Gly Ser Asp	Glu Gln Gly Cys Arg	Ile Ala Pro	
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Ser Gly Leu Leu Pro Ile Ala Arg Val Leu Thr Val Gly Ala Asp Arg
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Ile Pro Arg Ala Trp Leu Cys Asp Arg Glu Asp Asp Cys Gly Asp Gln
980 985 990

Thr Asp Glu Met Ala Ser Cys Glu Phe Pro Thr Cys Glu Pro Leu Thr
995 1000 1005

Gln Phe Val Cys Lys Ser Gly Arg Cys Ile Ser Ser Lys Trp His
1010 1015 1020

Cys Asp Ser Asp Asp Asp Cys Gly Asp Gly Ser Asp Glu Val Gly
1025 1030 1035

Cys Val His Ser Cys Phe Asp Asn Gln Phe Arg Cys Ser Ser Gly
1040 1045 1050

Arg Cys Ile Pro Gly His Trp Ala Cys Asp Gly Asp Asn Asp Cys
1055 1060 1065

Gly Asp Phe Ser Asp Glu Ala Gln Ile Asn Cys Thr Lys Glu Glu
1070 1075 1080

Ile His Ser Pro Ala Gly Cys Asn Gly Asn Glu Phe Gln Cys His
1085 1090 1095

1000 1005 1010 1015 1020 1025 1030 1035 1040 1045 1050 1055 1060 1065 1070 1075 1080 1085 1090 1095

Pro	Asp	Gly	Asn	Cys	Val	Pro	Asp	Leu	Trp	Arg	Cys	Asp	Gly	Glu
1100						1105					1110			
Lys	Asp	Cys	Glu	Asp	Gly	Ser	Asp	Glu	Lys	Gly	Cys	Asn	Gly	Thr
1115						1120					1125			
Ile	Arg	Leu	Cys	Asp	His	Lys	Thr	Lys	Phe	Ser	Cys	Trp	Ser	Thr
1130						1135					1140			
Gly	Arg	Cys	Ile	Asn	Lys	Ala	Trp	Val	Cys	Asp	Gly	Asp	Ile	Asp
1145						1150					1155			
Cys	Glu	Asp	Gln	Ser	Asp	Glu	Asp	Asp	Cys	Asp	Ser	Phe	Leu	Cys
1160						1165					1170			
Gly	Pro	Pro	Lys	His	Pro	Cys	Ala	Asn	Asp	Thr	Ser	Val	Cys	Leu
1175						1180					1185			
Gln	Pro	Glu	Lys	Leu	Cys	Asn	Gly	Lys	Lys	Asp	Cys	Pro	Asp	Gly
1190						1195					1200			
Ser	Asp	Glu	Gly	Tyr	Leu	Cys	Asp	Glu	Cys	Ser	Leu	Asn	Asn	Gly
1205						1210					1215			
Gly	Cys	Ser	Asn	His	Cys	Ser	Val	Val	Pro	Gly	Arg	Gly	Ile	Val
1220						1225					1230			
Cys	Ser	Cys	Pro	Glu	Gly	Leu	Gln	Leu	Asn	Lys	Asp	Asn	Lys	Thr
1235						1240					1245			
Cys	Glu	Ile	Val	Asp	Tyr	Cys	Ser	Asn	His	Leu	Lys	Cys	Ser	Gln
1250						1255					1260			
Val	Cys	Glu	Gln	His	Lys	His	Thr	Val	Lys	Cys	Ser	Cys	Tyr	Glu
1265						1270					1275			
Gly	Trp	Lys	Leu	Asp	Val	Asp	Gly	Glu	Ser	Cys	Thr	Ser	Val	Asp
1280						1285					1290			
Pro	Phe	Glu	Ala	Phe	Ile	Ile	Phe	Ser	Ile	Arg	His	Glu	Ile	Arg
1295						1300					1305			
Arg	Ile	Asp	Leu	His	Lys	Arg	Asp	Tyr	Ser	Leu	Leu	Val	Pro	Gly
1310						1315					1320			
Leu	Arg	Asn	Thr	Ile	Ala	Leu	Asp	Phe	His	Phe	Asn	Gln	Ser	Leu
1325						1330					1335			

Leu Tyr Trp Thr Asp Val Val Glu Asp Arg Ile Tyr Arg Gly Lys
1340 1345 1350

Leu Ser Glu Ser Gly Gly Val Ser Ala Ile Glu Val Val Val Glu
1355 1360 1365

His Gly Leu Ala Thr Pro Glu Gly Leu Thr Val Asp Trp Ile Ala
1370 1375 1380

Gly Asn Ile Tyr Trp Ile Asp Ser Asn Leu Asp Gln Ile Glu Val
1385 1390 1395

Ala Lys Leu Asp Gly Ser Leu Arg Thr Thr Leu Ile Ala Gly Ala
1400 1405 1410

Met Glu His Pro Arg Ala Ile Ala Leu Asp Pro Arg Tyr Gly Ile
1415 1420 1425

Leu Phe Trp Thr Asp Trp Asp Ala Asn Phe Pro Arg Ile Glu Ser
1430 1435 1440

Ala Ser Met Ser Gly Ala Gly Arg Lys Thr Ile Tyr Lys Asp Met
1445 1450 1455

Lys Thr Gly Ala Trp Pro Asn Gly Leu Thr Val Asp His Phe Glu
1460 1465 1470

Lys Arg Ile Val Trp Thr Asp Ala Arg Ser Asp Ala Ile Tyr Ser
1475 1480 1485

Ala Leu Tyr Asp Gly Thr Asn Met Ile Glu Ile Ile Arg Gly His
1490 1495 1500

Glu Tyr Leu Ser His Pro Phe Ala Val Ser Leu Tyr Gly Ser Glu
1505 1510 1515

Val Tyr Trp Thr Asp Trp Arg Thr Asn Thr Leu Ser Lys Ala Asn
1520 1525 1530

Lys Trp Thr Gly Gln Asn Val Ser Val Ile Gln Lys Thr Ser Ala
1535 1540 1545

Gln Pro Phe Asp Leu Gln Ile Tyr His Pro Ser Arg Gln Pro Gln
1550 1555 1560

Ala Pro Asn Pro Cys Ala Ala Asn Asp Gly Lys Gly Pro Cys Ser
1565 1570 1575

His Met Cys Leu Ile Asn His Asn Arg Ser Ala Ala Cys Ala Cys
1580 1585 1590

Pro His Leu Met Lys Leu Ser Ser Asp Lys Lys Thr Cys Tyr Glu
1595 1600 1605

Met Lys Lys Phe Leu Leu Tyr Ala Arg Arg Ser Glu Ile Arg Gly
1610 1615 1620

Val Asp Ile Asp Asn Pro Tyr Phe Asn Phe Ile Thr Ala Phe Thr
1625 1630 1635

Val Pro Asp Ile Asp Asp Val Thr Val Ile Asp Phe Asp Ala Ser
1640 1645 1650

Glu Glu Arg Leu Tyr Trp Thr Asp Ile Lys Thr Gln Thr Ile Lys
1655 1660 1665

Arg Ala Phe Ile Asn Gly Thr Gly Leu Glu Thr Val Ile Ser Arg
1670 1675 1680

Asp Ile Gln Ser Ile Arg Gly Leu Ala Val Asp Trp Val Ser Arg
1685 1690 1695

Asn Leu Tyr Trp Ile Ser Ser Glu Phe Asp Glu Thr Gln Ile Asn
1700 1705 1710

Val Ala Arg Leu Asp Gly Ser Leu Lys Thr Ser Ile Ile His Gly
1715 1720 1725

Ile Asp Lys Pro Gln Cys Leu Ala Ala His Pro Val Arg Gly Lys
1730 1735 1740

Leu Tyr Trp Thr Asp Gly Asn Thr Ile Asn Met Ala Asn Met Asp
1745 1750 1755

Gly Ser Asn Ser Lys Ile Leu Phe Gln Asn Gln Lys Glu Pro Val
1760 1765 1770

Gly Leu Ser Ile Asp Tyr Val Glu Asn Lys Leu Tyr Trp Ile Ser
1775 1780 1785

Ser Gly Asn Gly Thr Ile Asn Arg Cys Asn Leu Asp Gly Gly Asn
1790 1795 1800

Leu Glu Val Ile Glu Ser Met Lys Glu Glu Leu Thr Lys Ala Thr
1805 1810 1815

Ala	Leu	Thr	Ile	Met	Asp	Lys	Lys	Leu	Trp	Trp	Ala	Asp	Gln	Asn
1820						1825					1830			
Leu	Ala	Gln	Leu	Gly	Thr	Cys	Ser	Lys	Arg	Asp	Gly	Arg	Asn	Pro
1835						1840					1845			
Thr	Ile	Leu	Arg	Asn	Lys	Thr	Ser	Gly	Val	Val	His	Met	Lys	Val
1850						1855					1860			
Tyr	Asp	Lys	Glu	Ala	Gln	Gln	Gly	Ser	Asn	Ser	Cys	Gln	Leu	Asn
1865						1870					1875			
Asn	Gly	Gly	Cys	Ser	Gln	Leu	Cys	Leu	Pro	Thr	Ser	Glu	Thr	Thr
1880						1885					1890			
Arg	Thr	Cys	Met	Cys	Thr	Val	Gly	Tyr	Tyr	Leu	Gln	Lys	Asn	Arg
1895						1900					1905			
Met	Ser	Cys	Gln	Gly	Ile	Glu	Ser	Phe	Leu	Met	Tyr	Ser	Val	His
1910						1915					1920			
Glu	Gly	Ile	Arg	Gly	Ile	Pro	Leu	Glu	Pro	Ser	Asp	Lys	Met	Asp
1925						1930					1935			
Ala	Leu	Met	Pro	Ile	Ser	Gly	Thr	Ser	Phe	Ala	Val	Gly	Ile	Asp
1940						1945					1950			
Phe	His	Ala	Glu	Asn	Asp	Thr	Ile	Tyr	Trp	Thr	Asp	Met	Gly	Phe
1955						1960					1965			
Asn	Lys	Ile	Ser	Arg	Ala	Lys	Arg	Asp	Gln	Thr	Trp	Lys	Glu	Asp
1970						1975					1980			
Ile	Ile	Thr	Asn	Gly	Leu	Gly	Arg	Val	Glu	Gly	Ile	Ala	Val	Asp
1985						1990					1995			
Trp	Ile	Ala	Gly	Asn	Ile	Tyr	Trp	Thr	Asp	His	Gly	Phe	Asn	Leu
2000						2005					2010			
Ile	Glu	Val	Ala	Arg	Leu	Asn	Gly	Ser	Phe	Arg	Tyr	Val	Ile	Ile
2015						2020					2025			
Ser	Gln	Gly	Leu	Asp	Gln	Pro	Arg	Ser	Ile	Ala	Val	His	Pro	Glu
2030						2035					2040			
Lys	Gly	Leu	Leu	Phe	Trp	Thr	Glu	Trp	Gly	Gln	Met	Pro	Cys	Ile
2045						2050					2055			

Gly	Lys	Ala	Arg	Leu	Asp	Gly	Ser	Glu	Lys	Val	Val	Leu	Val	Ser
2060						2065					2070			
Met	Gly	Ile	Ala	Trp	Pro	Asn	Gly	Ile	Ser	Ile	Asp	Tyr	Glu	Glu
2075						2080					2085			
Asn	Lys	Leu	Tyr	Trp	Cys	Asp	Ala	Arg	Thr	Asp	Lys	Ile	Glu	Arg
2090						2095					2100			
Ile	Asp	Leu	Glu	Thr	Gly	Gly	Asn	Arg	Glu	Met	Val	Leu	Ser	Gly
2105						2110					2115			
Ser	Asn	Val	Asp	Met	Phe	Ser	Val	Ala	Val	Phe	Gly	Ala	Tyr	Ile
2120						2125					2130			
Tyr	Trp	Ser	Asp	Arg	Ala	His	Ala	Asn	Gly	Ser	Val	Arg	Arg	Gly
2135						2140					2145			
His	Lys	Asn	Asp	Ala	Thr	Glu	Thr	Ile	Thr	Met	Arg	Thr	Gly	Leu
2150						2155					2160			
Gly	Val	Asn	Leu	Lys	Glu	Val	Lys	Ile	Phe	Asn	Arg	Val	Arg	Glu
2165						2170					2175			
Lys	Gly	Thr	Asn	Val	Cys	Ala	Arg	Asp	Asn	Gly	Gly	Cys	Lys	Gln
2180						2185					2190			
Leu	Cys	Leu	Tyr	Arg	Gly	Asn	Ser	Arg	Arg	Thr	Cys	Ala	Cys	Ala
2195						2200					2205			
His	Gly	Tyr	Leu	Ala	Glu	Asp	Gly	Val	Thr	Cys	Leu	Arg	His	Glu
2210						2215					2220			
Gly	Tyr	Leu	Leu	Tyr	Ser	Gly	Arg	Thr	Ile	Leu	Lys	Ser	Ile	His
2225						2230					2235			
Leu	Ser	Asp	Glu	Thr	Asn	Leu	Asn	Ser	Pro	Ile	Arg	Pro	Tyr	Glu
2240						2245					2250			
Asn	Pro	Arg	Tyr	Phe	Lys	Asn	Val	Ile	Ala	Leu	Ala	Phe	Asp	Tyr
2255						2260					2265			
Asn	Gln	Arg	Arg	Lys	Gly	Thr	Asn	Arg	Ile	Phe	Tyr	Ser	Asp	Ala
2270						2275					2280			
His	Phe	Gly	Asn	Ile	Gln	Leu	Ile	Lys	Asp	Asn	Trp	Glu	Asp	Arg
2285						2290					2295			

Gln	Val	Ile	Val	Glu	Asn	Val	Gly	Ser	Val	Glu	Gly	Leu	Ala	Tyr
2300						2305					2310			
His	Arg	Ala	Trp	Asp	Thr	Leu	Tyr	Trp	Thr	Ser	Ser	Thr	Thr	Ser
2315						2320					2325			
Ser	Ile	Thr	Arg	His	Thr	Val	Asp	Gln	Thr	Arg	Pro	Gly	Ala	Phe
2330						2335					2340			
Asp	Arg	Glu	Ala	Val	Ile	Thr	Met	Ser	Glu	Asp	Asp	His	Pro	His
2345						2350					2355			
Val	Leu	Ala	Leu	Asp	Glu	Cys	Gln	Asn	Leu	Met	Phe	Trp	Thr	Asn
2360						2365					2370			
Trp	Asn	Glu	Gln	His	Pro	Ser	Ile	Met	Arg	Ser	Thr	Leu	Thr	Gly
2375						2380					2385			
Lys	Asn	Ala	Gln	Val	Val	Val	Ser	Thr	Asp	Ile	Leu	Thr	Pro	Asn
2390						2395					2400			
Gly	Leu	Thr	Ile	Asp	Tyr	Arg	Ala	Glu	Lys	Leu	Tyr	Phe	Ser	Asp
2405						2410					2415			
Gly	Ser	Leu	Gly	Lys	Ile	Glu	Arg	Cys	Glu	Tyr	Asp	Gly	Ser	Gln
2420						2425					2430			
Arg	His	Val	Ile	Val	Lys	Ser	Gly	Pro	Gly	Thr	Phe	Leu	Ser	Leu
2435						2440					2445			
Ala	Val	Tyr	Asp	Asn	Tyr	Ile	Phe	Trp	Ser	Asp	Trp	Gly	Arg	Arg
2450						2455					2460			
Ala	Ile	Leu	Arg	Ser	Asn	Lys	Tyr	Thr	Gly	Gly	Asp	Thr	Lys	Ile
2465						2470					2475			
Leu	Arg	Ser	Asp	Ile	Pro	His	Gln	Pro	Met	Gly	Ile	Ile	Ala	Val
2480						2485					2490			
Ala	Asn	Asp	Thr	Asn	Ser	Cys	Glu	Leu	Ser	Pro	Cys	Ala	Leu	Leu
2495						2500					2505			
Asn	Gly	Gly	Cys	His	Asp	Leu	Cys	Leu	Leu	Thr	Pro	Asn	Gly	Arg
2510						2515					2520			
Val	Asn	Cys	Ser	Cys	Arg	Gly	Asp	Arg	Ile	Leu	Leu	Glu	Asp	Asn
2525						2530					2535			

Arg 2540	Cys 2540	Val	Thr	Lys	Asn	Ser 2545	Ser	Cys	Asn	Ala	Tyr 2550	Ser	Glu	Phe
Glu 2555	Cys 2555	Gly	Asn	Gly	Glu	Cys 2560	Ile	Asp	Tyr	Gln	Leu 2565	Thr	Cys	Asp
Gly 2570	Ile 2570	Pro	His	Cys	Lys	Asp 2575	Lys	Ser	Asp	Glu	Lys 2580	Leu	Leu	Tyr
Cys 2585	Glu 2585	Asn	Arg	Ser	Cys	Arg 2590	Arg	Gly	Phe	Lys	Pro 2595	Cys	Tyr	Asn
Arg 2600	Arg 2600	Cys	Ile	Pro	His	Gly 2605	Lys	Leu	Cys	Asp	Gly 2610	Glu	Asn	Asp
Cys 2615	Gly 2615	Asp	Asn	Ser	Asp	Glu 2620	Leu	Asp	Cys	Lys	Val 2625	Ser	Thr	Cys
Ala 2630	Thr 2630	Val	Glu	Phe	Arg	Cys 2635	Ala	Asp	Gly	Thr	Cys 2640	Ile	Pro	Arg
Ser 2645	Ala 2645	Arg	Cys	Asn	Gln	Asn 2650	Ile	Asp	Cys	Ala	Asp 2655	Ala	Ser	Asp
Glu 2660	Lys 2660	Asn	Cys	Asn	Asn	Thr 2665	Asp	Cys	Thr	His	Phe 2670	Tyr	Lys	Leu
Gly 2675	Val 2675	Lys	Thr	Thr	Gly	Phe 2680	Ile	Arg	Cys	Asn	Ser 2685	Thr	Ser	Leu
Cys 2690	Val 2690	Leu	Pro	Thr	Trp	Ile 2695	Cys	Asp	Gly	Ser	Asn 2700	Asp	Cys	Gly
Asp 2705	Tyr 2705	Ser	Asp	Glu	Leu	Lys 2710	Cys	Pro	Val	Gln	Asn 2715	Lys	His	Lys
Cys 2720	Glu 2720	Glu	Asn	Tyr	Phe	Ser 2725	Cys	Pro	Ser	Gly	Arg 2730	Cys	Ile	Leu
Asn 2735	Thr 2735	Trp	Ile	Cys	Asp	Gly 2740	Gln	Lys	Asp	Cys	Glu 2745	Asp	Gly	Arg
Asp 2750	Glu 2750	Phe	His	Cys	Asp	Ser 2755	Ser	Cys	Ser	Trp	Asn 2760	Gln	Phe	Ala
Cys 2765	Ser 2765	Ala	Gln	Lys	Cys	Ile 2770	Ser	Lys	His	Trp	Ile 2775	Cys	Asp	Gly

Glu Asp Asp Cys Gly Asp Gly Leu Asp Glu Ser Asp Ser Ile Cys
2780 2785 2790

Gly Ala Ile Thr Cys Ala Ala Asp Met Phe Ser Cys Gln Gly Ser
2795 2800 2805

Arg Ala Cys Val Pro Arg His Trp Leu Cys Asp Gly Glu Arg Asp
2810 2815 2820

Cys Pro Asp Gly Ser Asp Glu Leu Ser Thr Ala Gly Cys Ala Pro
2825 2830 2835

Asn Asn Thr Cys Asp Glu Asn Ala Phe Met Cys His Asn Lys Val
2840 2845 2850

Cys Ile Pro Lys Gln Phe Val Cys Asp His Asp Asp Asp Cys Gly
2855 2860 2865

Asp Gly Ser Asp Glu Ser Pro Gln Cys Gly Tyr Arg Gln Cys Gly
2870 2875 2880

Thr Glu Glu Phe Ser Cys Ala Asp Gly Arg Cys Leu Leu Asn Thr
2885 2890 2895

Gln Trp Gln Cys Asp Gly Asp Phe Asp Cys Pro Asp His Ser Asp
2900 2905 2910

Glu Ala Pro Leu Asn Pro Lys Cys Lys Ser Ala Glu Gln Ser Cys
2915 2920 2925

Asn Ser Ser Phe Phe Met Cys Lys Asn Gly Arg Cys Ile Pro Ser
2930 2935 2940

Gly Gly Leu Cys Asp Asn Lys Asp Asp Cys Gly Asp Gly Ser Asp
2945 2950 2955

Glu Arg Asn Cys His Ile Asn Glu Cys Leu Ser Lys Lys Val Ser
2960 2965 2970

Gly Cys Ser Gln Asp Cys Gln Asp Leu Pro Val Ser Tyr Lys Cys
2975 2980 2985

Lys Cys Trp Pro Gly Phe Gln Leu Lys Asp Asp Gly Lys Thr Cys
2990 2995 3000

Val Asp Ile Asp Glu Cys Ser Ser Gly Phe Pro Cys Ser Gln Gln
3005 3010 3015

Cys	Ile	Asn	Thr	Tyr	Gly	Thr	Tyr	Lys	Cys	Leu	Cys	Thr	Asp	Gly
3020						3025					3030			
Tyr	Glu	Ile	Gln	Pro	Asp	Asn	Pro	Asn	Gly	Cys	Lys	Ser	Leu	Ser
3035						3040					3045			
Asp	Glu	Glu	Pro	Phe	Leu	Ile	Leu	Ala	Asp	His	His	Glu	Ile	Arg
3050						3055					3060			
Lys	Ile	Ser	Thr	Asp	Gly	Ser	Asn	Tyr	Thr	Leu	Leu	Lys	Gln	Gly
3065						3070					3075			
Leu	Asn	Asn	Val	Ile	Ala	Ile	Asp	Phe	Asp	Tyr	Arg	Glu	Glu	Phe
3080						3085					3090			
Ile	Tyr	Trp	Ile	Asp	Ser	Ser	Arg	Pro	Asn	Gly	Ser	Arg	Ile	Asn
3095						3100					3105			
Arg	Met	Cys	Leu	Asn	Gly	Ser	Asp	Ile	Lys	Val	Val	His	Asn	Thr
3110						3115					3120			
Ala	Val	Pro	Asn	Ala	Leu	Ala	Val	Asp	Trp	Ile	Gly	Lys	Asn	Leu
3125						3130					3135			
Tyr	Trp	Ser	Asp	Thr	Glu	Lys	Arg	Ile	Ile	Glu	Val	Ser	Lys	Leu
3140						3145					3150			
Asn	Gly	Leu	Tyr	Pro	Thr	Ile	Leu	Val	Ser	Lys	Arg	Leu	Lys	Phe
3155						3160					3165			
Pro	Arg	Asp	Leu	Ser	Leu	Asp	Pro	Gln	Ala	Gly	Tyr	Leu	Tyr	Trp
3170						3175					3180			
Ile	Asp	Cys	Cys	Glu	Tyr	Pro	His	Ile	Gly	Arg	Val	Gly	Met	Asp
3185						3190					3195			
Gly	Thr	Asn	Gln	Ser	Val	Val	Ile	Glu	Thr	Lys	Ile	Ser	Arg	Pro
3200						3205					3210			
Met	Ala	Leu	Thr	Ile	Asp	Tyr	Val	Asn	Arg	Arg	Leu	Tyr	Trp	Ala
3215						3220					3225			
Asp	Glu	Asn	His	Ile	Glu	Phe	Ser	Asn	Met	Asp	Gly	Ser	His	Arg
3230						3235					3240			
His	Lys	Val	Pro	Asn	Gln	Asp	Ile	Pro	Gly	Val	Ile	Ala	Leu	Thr
3245						3250					3255			

Leu	Phe	Glu	Asp	Tyr	Ile	Tyr	Trp	Thr	Asp	Gly	Lys	Thr	Lys	Ser
3260						3265					3270			
Leu	Ser	Arg	Ala	His	Lys	Thr	Ser	Gly	Ala	Asp	Arg	Leu	Ser	Leu
3275						3280					3285			
Ile	Tyr	Ser	Trp	His	Ala	Ile	Thr	Asp	Ile	Gln	Val	Tyr	His	Ser
3290						3295					3300			
Tyr	Arg	Gln	Pro	Asp	Val	Ser	Lys	His	Leu	Cys	Met	Ile	Asn	Asn
3305						3310					3315			
Gly	Gly	Cys	Ser	His	Leu	Cys	Leu	Leu	Ala	Pro	Gly	Lys	Thr	His
3320						3325					3330			
Thr	Cys	Ala	Cys	Pro	Thr	Asn	Phe	Tyr	Leu	Ala	Ala	Asp	Asn	Arg
3335						3340					3345			
Thr	Cys	Leu	Ser	Asn	Cys	Thr	Ala	Ser	Gln	Phe	Arg	Cys	Lys	Thr
3350						3355					3360			
Asp	Lys	Cys	Ile	Pro	Phe	Trp	Trp	Lys	Cys	Asp	Thr	Val	Asp	Asp
3365						3370					3375			
Cys	Gly	Asp	Gly	Ser	Asp	Glu	Pro	Asp	Asp	Cys	Pro	Glu	Phe	Arg
3380						3385					3390			
Cys	Gln	Pro	Gly	Arg	Phe	Gln	Cys	Gly	Thr	Gly	Leu	Cys	Ala	Leu
3395						3400					3405			
Pro	Ala	Phe	Ile	Cys	Asp	Gly	Glu	Asn	Asp	Cys	Gly	Asp	Asn	Ser
3410						3415					3420			
Asp	Glu	Leu	Asn	Cys	Asp	Thr	His	Val	Cys	Leu	Ser	Gly	Gln	Phe
3425						3430					3435			
Lys	Cys	Thr	Lys	Asn	Gln	Lys	Cys	Ile	Pro	Val	Asn	Leu	Arg	Cys
3440						3445					3450			
Asn	Gly	Gln	Asp	Asp	Cys	Gly	Asp	Glu	Glu	Asp	Glu	Arg	Asp	Cys
3455						3460					3465			
Pro	Glu	Asn	Ser	Cys	Ser	Pro	Asp	Tyr	Phe	Gln	Cys	Lys	Thr	Thr
3470						3475					3480			
Lys	His	Cys	Ile	Ser	Lys	Leu	Trp	Val	Cys	Asp	Glu	Asp	Pro	Asp
3485						3490					3495			

Cys	Ala	Asp	Ala	Ser	Asp	Glu	Ala	Asn	Cys	Asp	Lys	Lys	Thr	Cys
3500						3505					3510			
Gly	Pro	His	Glu	Phe	Gln	Cys	Lys	Asn	Asn	Asn	Cys	Ile	Pro	Asp
3515						3520					3525			
His	Trp	Arg	Cys	Asp	Ser	Gln	Asn	Asp	Cys	Ser	Asp	Asn	Ser	Asp
3530						3535					3540			
Glu	Glu	Asn	Cys	Lys	Pro	Gln	Thr	Cys	Thr	Leu	Lys	Asp	Phe	Leu
3545						3550					3555			
Cys	Ala	Asn	Gly	Asp	Cys	Val	Ser	Ser	Arg	Phe	Trp	Cys	Asp	Gly
3560						3565					3570			
Asp	Phe	Asp	Cys	Ala	Asp	Gly	Ser	Asp	Glu	Arg	Asn	Cys	Glu	Thr
3575						3580					3585			
Ser	Cys	Ser	Lys	Asp	Gln	Phe	Arg	Cys	Ser	Asn	Gly	Gln	Cys	Ile
3590						3595					3600			
Pro	Ala	Lys	Trp	Lys	Cys	Asp	Gly	His	Glu	Asp	Cys	Lys	Tyr	Gly
3605						3610					3615			
Glu	Asp	Glu	Lys	Ser	Cys	Glu	Pro	Ala	Ser	Pro	Thr	Cys	Ser	Ser
3620						3625					3630			
Arg	Glu	Tyr	Ile	Cys	Ala	Ser	Asp	Gly	Cys	Ile	Ser	Ala	Ser	Leu
3635						3640					3645			
Lys	Cys	Asn	Gly	Glu	Tyr	Asp	Cys	Ala	Asp	Gly	Ser	Asp	Glu	Met
3650						3655					3660			
Asp	Cys	Val	Thr	Glu	Cys	Lys	Glu	Asp	Gln	Phe	Arg	Cys	Lys	Asn
3665						3670					3675			
Lys	Ala	His	Cys	Ile	Pro	Ile	Arg	Trp	Leu	Cys	Asp	Gly	Ile	His
3680						3685					3690			
Asp	Cys	Val	Asp	Gly	Ser	Asp	Glu	Glu	Asn	Cys	Glu	Arg	Gly	Gly
3695						3700					3705			
Asn	Ile	Cys	Arg	Ala	Asp	Glu	Phe	Leu	Cys	Asn	Asn	Ser	Leu	Cys
3710						3715					3720			
Lys	Leu	His	Phe	Trp	Val	Cys	Asp	Gly	Glu	Asp	Asp	Cys	Gly	Asp
3725						3730					3735			

Asn Ser	Asp Glu Ala Pro Asp	Met Cys Val Lys Phe	Leu Cys Pro
3740	3745	3750	
Ser Thr	Arg Pro His Arg Cys	Arg Asn Asn Arg Ile	Cys Leu Gln
3755	3760	3765	
Ser Glu	Gln Met Cys Asn Gly	Ile Asp Glu Cys Gly	Asp Asn Ser
3770	3775	3780	
Asp Glu	Asp His Cys Gly Gly	Lys Leu Thr Tyr Lys	Ala Arg Pro
3785	3790	3795	
Cys Lys	Lys Asp Glu Phe Ala	Cys Ser Asn Lys Lys	Cys Ile Pro
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Met Asp	Leu Gln Cys Asp Arg	Leu Asp Asp Cys Gly	Asp Gly Ser
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Asp Glu	Gln Gly Cys Arg Ile	Ala Pro Thr Glu Tyr	Thr Cys Glu
3830	3835	3840	
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Lys Thr	Ser Val Phe Cys Arg	Cys Lys Pro Gly Phe	Gln Arg Asn
3860	3865	3870	
Met Lys	Asn Arg Gln Cys Glu	Asp Leu Asn Glu Cys	Leu Val Phe
3875	3880	3885	
Gly Thr	Cys Ser His Gln Cys	Ile Asn Val Glu Gly	Ser Tyr Lys
3890	3895	3900	
Cys Val	Cys Asp Gln Asn Phe	Gln Glu Arg Asn Asn	Thr Cys Ile
3905	3910	3915	
Ala Glu	Gly Ser Glu Asp Gln	Val Leu Tyr Ile Ala	Asn Asp Thr
3920	3925	3930	
Asp Ile	Leu Gly Phe Ile Tyr	Pro Phe Asn Tyr Ser	Gly Asp His
3935	3940	3945	
Gln Gln	Ile Ser His Ile Glu	His Asn Ser Arg Ile	Thr Gly Met
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Asp Val	Tyr Tyr Gln Arg Asp	Met Ile Ile Trp Ser	Thr Gln Phe
3965	3970	3975	

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Leu Leu Val Thr Leu Ile Thr Thr Leu Val Ile Gly Leu Val Leu
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Cys Lys Arg Lys Arg Arg Thr Lys Thr Ile Arg Arg Gln Pro Ile
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Ile Asn Gly Gly Ile Asn Val Glu Ile Gly Asn Pro Ser Tyr Asn
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Met Tyr Glu Val Asp His Asp His Asn Asp Gly Gly Leu Leu Asp
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Pro Gly Phe Met Ile Asp Pro Thr Lys Ala Arg Tyr Ile Gly Gly
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Gly Pro Ser Ala Phe Lys Leu Pro His Thr Ala Pro Pro Ile Tyr
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Leu Asn Ser Asp Leu Lys Gly Pro Leu Thr Ala Gly Pro Thr Asn
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Tyr Ser Asn Pro Val Tyr Ala Lys Leu Tyr Met Asp Gly Gln Asn
4595 4600 4605

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Trp 210	Leu	Trp	Met	Asp	Gly	Thr 215	Pro	Phe	Thr	Ser	Glu 220	Leu	Phe	His	Ile
Ile 225	Ile	Asp	Val	Thr 230	Ser	Pro	Arg	Ser	Arg	Asp 235	Cys	Val	Ala	Ile	Leu
Asn	Gly	Met	Ile 245	Phe	Ser	Lys	Asp	Cys	Lys 250	Glu	Leu	Lys	Arg	Cys 255	Val

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<212> PRT
<213> Homo sapiens
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Pro	Glu	Pro 35	Arg	Arg	Thr	Glu	His 40	Arg	Ala	Pro	Ser	Ser 45	Thr	Trp	Arg
Pro 50	Val	Ala	Leu	Thr	Leu	Leu 55	Thr	Leu	Cys	Leu 60	Val	Leu	Leu	Ile	Gly
Leu 65	Ala	Ala	Leu	Gly	Leu 70	Leu	Phe	Phe	Gln	Tyr 75	Tyr	Gln	Leu	Ser	Asn 80
Thr	Gly	Gln	Asp	Thr 85	Ile	Ser	Gln	Met	Glu 90	Glu	Arg	Leu	Gly	Asn 95	Thr
Ser	Gln	Glu	Leu 100	Gln	Ser	Leu	Gln	Val 105	Gln	Asn	Ile	Lys	Leu 110	Ala	Gly
Ser	Leu	Gln 115	His	Val	Ala	Glu	Lys 120	Leu	Cys	Arg	Glu	Leu 125	Tyr	Asn	Lys

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Ser Leu Arg Gln Leu Pro His Met Gly Glu Ser Ala Ala Ala His Arg
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Cys Ser Pro Cys Thr Glu Gln Trp Lys Trp His Gly Asp Asn Cys Tyr
165 170 175

Gln Phe Tyr Lys Asp Ser Lys Ser Trp Glu Asp Cys Lys Tyr Phe Cys
180 185 190

Leu Ser Glu Asn Ser Thr Met Leu Lys Ile Asn Lys Gln Glu Asp Leu
195 200 205

Glu Phe Ala Ala Ser Gln Ser Tyr Ser Glu Phe Phe Tyr Ser Tyr Trp
210 215 220

Thr Gly Leu Leu Arg Pro Asp Ser Gly Lys Ala Trp Leu Trp Met Asp
225 230 235 240

Gly Thr Pro Phe Thr Ser Glu Leu Phe His Ile Ile Ile Asp Val Thr
245 250 255

Ser Pro Arg Ser Arg Asp Cys Val Ala Ile Leu Asn Gly Met Ile Phe
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<211> 2714

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Ile Leu Cys Arg Glu Leu Gly Phe Thr Glu Ala Thr Gly Trp Thr His
85 90 95
Ser Ala Lys Tyr Gly Pro Gly Thr Gly Arg Ile Trp Leu Asp Asn Leu
100 105 110
Ser Cys Ser Gly Thr Glu Gln Ser Val Thr Glu Cys Ala Ser Arg Gly
115 120 125
Trp Gly Asn Ser Asp Cys Thr His Asp Glu Asp Ala Gly Val Ile Cys
130 135 140
Lys Asp Gln Arg Leu Pro Gly Phe Ser Asp Ser Asn Val Ile Glu Val
145 150 155 160
Glu His His Leu Gln Val Glu Glu Val Arg Ile Arg Pro Ala Val Gly
165 170 175
Trp Gly Arg Arg Pro Leu Pro Val Thr Glu Gly Leu Val Glu Val Arg
180 185 190
Leu Pro Asp Gly Trp Ser Gln Val Cys Asp Lys Gly Trp Ser Ala His
195 200 205
Asn Ser His Val Val Cys Gly Met Leu Gly Phe Pro Ser Glu Lys Arg
210 215 220
Val Asn Ala Ala Phe Tyr Arg Lys Leu Arg Lys Arg Ala Ala Lys Val
225 230 235 240
Ser Ala Arg His Pro Lys Pro Leu Gly Arg Leu Leu Ala Gln Arg Gln
245 250 255
Gln His Ser Phe Gly Leu His Gly Val Ala Cys Val Gly Thr Glu Ala

[illegible]

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<210> 40
<211> 1877
<212> DNA
<213> Homo sapiens
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gtcttctcag agcaggtaat ggcaagcatg gctgccgtgc tcacctgggc tctggctctt 180
ctttcagcgt tttcggccac ccaggcacgg aaaggcttct gggactactt cagccagacc 240
agcggggaca aaggcaggtt ggagcagatc catcagcaga agatggctcg cgagcccgcg 300
accctgaaag acagccttga gcaagacctc aacaatatga acaagttcct ggaaaagctg 360
aggcctctga gtgggagcga ggctcctcgg ctcccacagg acccggtggg catgcggcgg 420
cagctgcagg aggagttaga ggaggtgaag gctcgcctcc agccctacat ggcagaggcg 480
cacgagctgg tgggctgga tttggagggc ttgcggcagc aactgaagcc ctacacgatg 540
gatctgatgg agcaggtggc cctgcgcgtg caggagctgc aggagcagtt gcgcgtggtg 600
ggggaagaca ccaaggccca gttgctgggg ggcgtggacg aggccttgggc tttgctgcag 660

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ggactgcaga gccgcgtggt gcaccacacc ggccgcttca aagagctctt ccaccatac 720
gccgagagcc tggtagcgcg catcgggcgc cacgtgcagg agctgcaccg cagtgtggct 780
ccgcacgccc ccgccagccc cgcgcgcctc agtcgctgcg tgcaggtgct ctcccgaag 840
ctcacgctca aggccaaggc cctgcacgca cgcattccagc agaacctgga ccagctgcgc 900
gaagagctca gcagagcctt tgcaggcact gggactgagg aaggggcccgg cccggacccc 960
cagatgctct ccgaggaggt gcgccagcga cttcaggctt tccgccagga cacctacctg 1020
cagatagctg ccttcactcg cgccatcgac caggagactg aggaggtcca gcagcagctg 1080
gcgccacctc caccaggcca cagtgccttc gcccagagt ttcaacaaac agacagtggc 1140
aaggttctga gcaagctgca ggcccgtctg gatgacctgt gggaagacat cactcacagc 1200
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<210> 41
<211> 400
<212> PRT
<213> Homo sapiens

<400> 41

Met Asn Lys Lys Lys Pro Leu His Ser Lys Ser Ser Arg Ile His Gln
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Gln Ile Ile Val Gln Leu Asp Ser Leu Pro Pro Pro Val Phe Ser Glu
20 25 30
Gln Val Met Ala Ser Met Ala Ala Val Leu Thr Trp Ala Leu Ala Leu
35 40 45
Leu Ser Ala Phe Ser Ala Thr Gln Ala Arg Lys Gly Phe Trp Asp Tyr
50 55 60
Phe Ser Gln Thr Ser Gly Asp Lys Gly Arg Val Glu Gln Ile His Gln

65	70	75	80
Gln Lys Met Ala Arg	Glu Pro Ala Thr	Leu Lys Asp Ser	Leu Glu Gln
	85	90	95
Asp Leu Asn Asn Met	Asn Lys Phe	Leu Glu Lys Leu Arg	Pro Leu Ser
	100	105	110
Gly Ser Glu Ala Pro Arg	Leu Pro Gln Asp	Pro Val Gly Met	Arg Arg
	115	120	125
Gln Leu Gln Glu Glu	Leu Glu Glu Val	Lys Ala Arg	Leu Gln Pro Tyr
	130	135	140
Met Ala Glu Ala His	Glu Leu Val Gly	Trp Asn Leu Glu	Gly Leu Arg
	145	150	155
Gln Gln Leu Lys Pro	Tyr Thr Met Asp	Leu Met Glu Gln	Val Ala Leu
	165	170	175
Arg Val Gln Glu Leu	Gln Glu Gln Leu	Arg Val Val Gly	Glu Asp Thr
	180	185	190
Lys Ala Gln Leu Leu	Gly Gly Val Asp	Glu Ala Trp Ala	Leu Leu Gln
	195	200	205
Gly Leu Gln Ser Arg	Val Val His His	Thr Gly Arg Phe	Lys Glu Leu
	210	215	220
Phe His Pro Tyr Ala	Glu Ser Leu Val	Ser Gly Ile Gly	Arg His Val
	225	230	235
Gln Glu Leu His Arg	Ser Val Ala Pro	His Ala Pro Ala	Ser Pro Ala
	245	250	255
Arg Leu Ser Arg Cys	Val Gln Val Leu	Ser Arg Lys Leu	Thr Leu Lys
	260	265	270
Ala Lys Ala Leu His	Ala Arg Ile Gln	Gln Asn Leu Asp	Gln Leu Arg
	275	280	285
Glu Glu Leu Ser Arg	Ala Phe Ala Gly	Thr Gly Thr Glu	Glu Gly Ala
	290	295	300
Gly Pro Asp Pro Gln	Met Leu Ser Glu	Glu Val Arg Gln	Arg Leu Gln
	305	310	315
Ala Phe Arg Gln Asp	Thr Tyr Leu Gln	Ile Ala Ala Phe	Thr Arg Ala
	325	330	335
Ile Asp Gln Glu Thr	Glu Glu Val Gln	Gln Gln Leu Ala	Pro Pro Pro
	340	345	350
Pro Gly His Ser Ala	Phe Ala Pro Glu	Phe Gln Gln Thr	Asp Ser Gly
	355	360	365
Lys Val Leu Ser Lys	Leu Gln Ala Arg	Leu Asp Asp Leu	Trp Glu Asp
	370	375	380
Ile Thr His Ser Leu	His Asp Gln Gly	His Ser His Leu	Gly Asp Pro
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			400

<211> 2128
<212> DNA
<213> Homo sapiens

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aagaaacgct tcaactgaaga agtcattgaa tacttccaga agaaagttag cccagtgcatt 240
ctgaaaatcc tgctgactag cgatgaagcc tggaagagat ttgtgcgtgt ggctgaattg 300
cccagggaag aggcagatgc tctctatgaa gctctgaaga atcttacacc atatgtgact 360
attgaggaca aagacatgca gcaaaaagaa cagcagttta gggagtgggt tttgaaagag 420
tttctcctcaa tcagatggaa gattcaggag tccatagaaa ggcttcgtgt cattgcaaat 480
gagattgaaa aggtccacag aggctgcgtc atcgccaatg tgggtgtctgg ctccactggc 540
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gtggagaaca catacacaag gtcagcagaa ctcacagcca gcaggctgac tgcaaccagc 720
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tttgcaattg attttgacga agccacaaaa atgattgcca atgatgtcca tacactcagg 840
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gttgagacac tgagaacacg tggggccccc acccgatag tgagaaaagt agcccggaac 960
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atctttgtga cccacaccct attcatacac tccctcccct tttgaaagtc cctaataaaa 2040
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<210> 43
<211> 348
<212> PRT
<213> Homo sapiens

<400> 43

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His Pro Gly Trp Thr Val Ala Gly Gln Phe Gln Glu Lys Lys Arg Phe
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Thr Glu Glu Val Ile Glu Tyr Phe Gln Lys Lys Val Ser Pro Val His
35 40 45
Leu Lys Ile Leu Leu Thr Ser Asp Glu Ala Trp Lys Arg Phe Val Arg
50 55 60
Val Ala Glu Leu Pro Arg Glu Glu Ala Asp Ala Leu Tyr Glu Ala Leu
65 70 75 80
Lys Asn Leu Thr Pro Tyr Val Thr Ile Glu Asp Lys Asp Met Gln Gln
85 90 95
Lys Glu Gln Gln Phe Arg Glu Trp Phe Leu Lys Glu Phe Pro Gln Ile
100 105 110
Arg Trp Lys Ile Gln Glu Ser Ile Glu Arg Leu Arg Val Ile Ala Asn
115 120 125
Glu Ile Glu Lys Val His Arg Gly Cys Val Ile Ala Asn Val Val Ser
130 135 140
Gly Ser Thr Gly Ile Leu Ser Val Ile Gly Val Met Leu Ala Pro Phe
145 150 155 160
Thr Ala Gly Leu Ser Leu Ser Ile Thr Ala Ala Gly Val Gly Leu Gly
165 170 175
Ile Ala Ser Ala Thr Ala Gly Ile Ala Ser Ser Ile Val Glu Asn Thr
180 185 190
Tyr Thr Arg Ser Ala Glu Leu Thr Ala Ser Arg Leu Thr Ala Thr Ser
195 200 205
Thr Asp Gln Leu Glu Ala Leu Arg Asp Ile Leu His Asp Ile Thr Pro
210 215 220

Asn Val Leu Ser Phe Ala Leu Asp Phe Asp Glu Ala Thr Lys Met Ile
 225 230 235 240

Ala Asn Asp Val His Thr Leu Arg Arg Ser Lys Ala Thr Val Gly Arg
 245 250 255

Pro Leu Ile Ala Trp Arg Tyr Val Pro Ile Asn Val Val Glu Thr Leu
 260 265 270

Arg Thr Arg Gly Ala Pro Thr Arg Ile Val Arg Lys Val Ala Arg Asn
 275 280 285

Leu Gly Lys Ala Thr Ser Gly Val Leu Val Val Leu Asp Val Val Asn
 290 295 300

Leu Val Gln Asp Ser Leu Asp Leu His Lys Gly Ala Lys Ser Glu Ser
 305 310 315 320

Ala Glu Ser Leu Arg Gln Trp Ala Gln Glu Leu Glu Glu Asn Leu Asn
 325 330 335

Glu Leu Thr His Ile His Gln Ser Leu Lys Ala Gly
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<210> 44
 <211> 988
 <212> DNA
 <213> Homo sapiens

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 <221> misc_feature
 <223> n = a or c or g or t

<220>
 <221> CDS
 <222> (129)..(971)

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agctcacagt agccccggcgg cccagggcaa tccgaccaca tttcactctc accgctgtag 120

gaatccag atg cag gcc aag tac agc agc acg agg gac atg ctg gat gat 170
 Met Gln Ala Lys Tyr Ser Ser Thr Arg Asp Met Leu Asp Asp
 1 5 10

gat ggg gac acc acc atg agc ctg cat tct caa gcc tct gcc aca act 218
 Asp Gly Asp Thr Thr Met Ser Leu His Ser Gln Ala Ser Ala Thr Thr
 15 20 25 30

cgg cat cca gag ccc cgg cgc aca gtt ttt cag tac tac cag ctc tcc 266
 Arg His Pro Glu Pro Arg Arg Thr Val Phe Gln Tyr Tyr Gln Leu Ser
 35 40 45

aat act ggt caa gac acc att tct caa atg gaa gaa aga tta gga aat 314
 Asn Thr Gly Gln Asp Thr Ile Ser Gln Met Glu Glu Arg Leu Gly Asn
 50 55 60

acg tcc caa gag ttg caa tct ctt caa gtc cag aat ata aag ctt gca 362
 Thr Ser Gln Glu Leu Gln Ser Leu Gln Val Gln Asn Ile Lys Leu Ala
 65 70 75

gga agt ctg cag cat gtg gct gaa aaa ctc tgt cgt gag ctg tat aac	410
Gly Ser Leu Gln His Val Ala Glu Lys Leu Cys Arg Glu Leu Tyr Asn	
80 85 90	
aaa gct gga ggc tat aca aga aac atg gtg cca gca tct gct tct tct	458
Lys Ala Gly Gly Tyr Thr Arg Asn Met Val Pro Ala Ser Ala Ser Ser	
95 100 105 110	
gag agc ctc agg cag ctt cca cac atg ggg gaa agt gca gca gca cac	506
Glu Ser Leu Arg Gln Leu Pro His Met Gly Glu Ser Ala Ala Ala His	
115 120 125	
agg tgc agc cct tgt aca gaa caa tgg aaa tgg cat gga gac aat tgc	554
Arg Cys Ser Pro Cys Thr Glu Gln Trp Lys Trp His Gly Asp Asn Cys	
130 135 140	
tac cag ttc tat aaa gac agc aaa agt tgg gag gac tgt aaa tat ttc	602
Tyr Gln Phe Tyr Lys Asp Ser Lys Ser Trp Glu Asp Cys Lys Tyr Phe	
145 150 155	
tgc ctt agt gaa aac tct acc atg ctg aag ata aac aaa caa gaa gac	650
Cys Leu Ser Glu Asn Ser Thr Met Leu Lys Ile Asn Lys Gln Glu Asp	
160 165 170	
ctg gaa ttt gcc gcg tct cag agc tac tct gag ttt ttc tac tct tat	698
Leu Glu Phe Ala Ala Ser Gln Ser Tyr Ser Glu Phe Phe Tyr Ser Tyr	
175 180 185 190	
tgg aca ggg ctt ttg cgc cct gac agt ggc aag gcc tgg ctg tgg atg	746
Trp Thr Gly Leu Leu Arg Pro Asp Ser Gly Lys Ala Trp Leu Trp Met	
195 200 205	
gat gga acc cct ttc act tct gaa ctg ttc cat att ata ata gat gtc	794
Asp Gly Thr Pro Phe Thr Ser Glu Leu Phe His Ile Ile Ile Asp Val	
210 215 220	
acc agc cca aga agc aga gac tgt gtg gcc atc ctt aat ggg atg atc	842
Thr Ser Pro Arg Ser Arg Asp Cys Val Ala Ile Leu Asn Gly Met Ile	
225 230 235	
ttc tca aag gac tgc aaa gaa ttg aag cgt tgt gtc tgt gag aga agg	890
Phe Ser Lys Asp Cys Lys Glu Leu Lys Arg Cys Val Cys Glu Arg Arg	
240 245 250	
gca gga atg gtg aag cca gag agc ctc cat gtc ccc cct gaa aca tta	938
Ala Gly Met Val Lys Pro Glu Ser Leu His Val Pro Pro Glu Thr Leu	
255 260 265 270	
ggc gaa ggt gac atg cat cat cat cat cat cat tagcctaggt tctagac	988
Gly Glu Gly Asp Met His His His His His His	
275 280	

<210> 45

<211> 281

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> n = a or c or g or t

<400> 45

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Asp Thr Thr Met Ser Leu His Ser Gln Ala Ser Ala Thr Thr Arg His
20 25 30

Pro Glu Pro Arg Arg Thr Val Phe Gln Tyr Tyr Gln Leu Ser Asn Thr
35 40 45

Gly Gln Asp Thr Ile Ser Gln Met Glu Glu Arg Leu Gly Asn Thr Ser
50 55 60

Gln Glu Leu Gln Ser Leu Gln Val Gln Asn Ile Lys Leu Ala Gly Ser
65 70 75 80

Leu Gln His Val Ala Glu Lys Leu Cys Arg Glu Leu Tyr Asn Lys Ala
85 90 95

Gly Gly Tyr Thr Arg Asn Met Val Pro Ala Ser Ala Ser Ser Glu Ser
100 105 110

Leu Arg Gln Leu Pro His Met Gly Glu Ser Ala Ala Ala His Arg Cys
115 120 125

Ser Pro Cys Thr Glu Gln Trp Lys Trp His Gly Asp Asn Cys Tyr Gln
130 135 140

Phe Tyr Lys Asp Ser Lys Ser Trp Glu Asp Cys Lys Tyr Phe Cys Leu
145 150 155 160

Ser Glu Asn Ser Thr Met Leu Lys Ile Asn Lys Gln Glu Asp Leu Glu
165 170 175

Phe Ala Ala Ser Gln Ser Tyr Ser Glu Phe Phe Tyr Ser Tyr Trp Thr
180 185 190

Gly Leu Leu Arg Pro Asp Ser Gly Lys Ala Trp Leu Trp Met Asp Gly
195 200 205

Thr Pro Phe Thr Ser Glu Leu Phe His Ile Ile Ile Asp Val Thr Ser
210 215 220

Pro Arg Ser Arg Asp Cys Val Ala Ile Leu Asn Gly Met Ile Phe Ser
225 230 235 240

Lys Asp Cys Lys Glu Leu Lys Arg Cys Val Cys Glu Arg Arg Ala Gly
245 250 255

[illegible]